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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:27:07 ; Search time 111.01 seconds
(without alignments)
501.665 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQQSGGLVQPGRLRL.....CQQLISYPLTFGGGKVEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 698052 seqs, 231078099 residues

Total number of hits satisfying chosen parameters: 698052

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1011.5	79.1	244	5	US-09-791-537-121728 Sequence 121728,
2	1001	78.3	240	5	US-09-791-537-22737 Sequence 22737, A
3	993	77.7	242	5	US-09-791-537-115236 Sequence 115236,
4	992	77.6	240	5	US-09-511-939-2 Sequence 2, Appli
5	992	77.6	240	5	US-09-968-561A-2 Sequence 2, Appli
6	991	77.5	239	5	US-09-791-537-121731 Sequence 121731,
7	938	73.4	248	5	US-09-791-537-115235 Sequence 115235,
8	901.5	70.5	240	6	US-10-127-890-148 Sequence 148, App
9	898.5	70.3	243	5	US-09-791-537-34222 Sequence 34222, A
10	888.5	69.5	224	5	US-09-791-537-128071 Sequence 128071,
11	886	69.3	232	5	US-09-791-537-128029 Sequence 128029,
12	885.5	69.3	243	5	US-09-791-537-9775 Sequence 9775, Ap
13	882	69.0	243	5	US-09-791-537-18026 Sequence 18026, A
14	880	68.9	232	5	US-09-791-537-128028 Sequence 128028,
15	878	68.7	244	5	US-09-791-537-22734 Sequence 22734, A
16	873	68.3	248	6	US-10-113-996-22 Sequence 22, Appl
17	871.5	68.2	229	5	US-09-791-537-128087 Sequence 128087,
18	871.5	68.2	229	5	US-09-791-537-131629 Sequence 131629,
19	869.5	68.0	268	5	US-09-791-537-850 Sequence 850, App
20	869	68.0	240	1	PCT-US02-16106-22 Sequence 22, Appl
21	869	68.0	240	6	US-10-151-882-22 Sequence 22, Appl
22	865.5	67.7	238	5	US-09-791-537-78382 Sequence 78382, A
23	864	67.6	248	6	US-10-113-996-23 Sequence 23, Appl
24	861.5	67.4	241	1	PCT-US02-16106-21 Sequence 21, Appl
25	861.5	67.4	241	6	US-10-151-882-21 Sequence 21, Appl
26	860.5	67.3	238	5	US-09-791-537-78362, A

27	858.5	67.2	238	5	US-09-791-537-78383 Sequence 78383, A
28	857.5	67.1	238	5	US-09-791-537-78381 Sequence 78381, A
29	857.5	67.1	239	1	PCT-US02-16106-23 Sequence 23, Appl
30	857.5	67.1	239	6	US-10-151-882-23 Sequence 23, Appl
31	854.5	66.9	238	5	US-09-791-537-78345 Sequence 78345, A
32	854.5	66.9	238	5	US-09-791-537-78380 Sequence 78380, A
33	851.5	66.6	238	5	US-09-791-537-78364 Sequence 78364, A
34	851.5	66.6	238	5	US-09-791-537-78365 Sequence 78365, A
35	849	66.4	232	5	US-09-791-537-128045 Sequence 128045,
36	848.5	66.4	238	5	US-09-791-537-78361 Sequence 78361, A
37	846.5	66.2	243	5	US-09-791-537-55358 Sequence 55358, A
38	846	66.2	248	5	US-09-791-537-55353 Sequence 55353, A
39	843	66.0	240	6	US-10-110-174-2 Sequence 2, Appli
40	842.5	65.9	238	5	US-09-791-537-78827 Sequence 78827, A
41	828.5	64.8	272	5	US-09-417-478-183 Sequence 183, App
42	823	64.4	240	5	US-09-791-537-138788 Sequence 138788,
43	819.5	64.1	277	5	US-09-522-727D-54 Sequence 54, Appl
44	815.5	63.8	294	5	US-09-661-992-100 Sequence 100, App
45	815.5	63.8	732	5	US-09-661-992-90 Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-09-791-537-121728
; Sequence 121728, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 121728
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-121728

Query Match	79.1%;	Score	1011.5;	DB 5;	Length	244;			
Best Local Similarity	79.5%;	Pred. NO.	1.8e-53;						
Matches	194;	Conservative	21;	Mismatches	26;	Indels	3;	Gaps	2;
QY	1	QVRLQQSGGGLVQPGRLRLSCAASGFTDDYAMHWVRQAPGKLEWVSGMTWNSGSIGY	60						
Db	1	QVQLVQSGGGLVQHGGSLRLSCAASGFTSSYEMNWRQAPGKLEWVSGISGGSTYY	60						
QY	61	ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREP--HNTD-AFDINGRGTLTVT	117						
Db	61	ADSVKGRFTISRDNKNTLYLQMNRLRAEDTAVYYCARDNGWELTDWYFDLWGRGTMVT	120						
QY	118	SSGGSGGPGGGSGGSDVVMVTQSPFLSAFVGDITITCRASQGIYNYLAWYQKPGKA	177						
Db	121	SSGGSGGSGGGSGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHNLAWYQKPGKA	180						
QY	178	PKLLIYAASTLQSGVPSRFRSGSGSGTEFTLTISLQPEDFGTYCQQLISYPLTFGGGTK	237						
Db	181	PKLLIYKASSLASGAPSRFRSGSGSGTGDTLTISLQPDDEFATYYCQQYSNYPLTFGGGTK	240						
QY	238	VEIK	241						
Db	241	LEIK	244						

RESULT 2
US-09-791-537-22737
; Sequence 22737, Application US/09791537

GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22737
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-22737

Query Match 78.3%; Score 1001; DB 5; Length 240;
Best Local Similarity 78.8%; Pred. No. 7.4e-53;
Matches 190; Conservative 22; Mismatches 27; Indels 2; Gaps 1;
QY 1 QVRLQSGGGLVQPGSLRLSCLAAAGTFFDDYAMHWRQAPGKGLWVSGMTWNSGSIGY 60
Db 1 QVQLVQSGGGLVQPGSLRLSCLAAAGTFFSSYGMHWRQAPGKGLWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTSSG 120
Db 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARD--WGDSLDPWKGTLVTSSG 118
QY 121 GGGPGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKPGKAPKL 180
Db 119 GGGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYRWLAWYQKPGKAPKL 178
QY 181 LIYAASLTQSGVPSRFSFGSGSGTEFTLTISLQPEDFGTYCCQLISYPLTFGGGKVEI 240
Db 179 LIYKASSLASRAPSRFSFGSGSGTDFTLTISLQPDDEFATYYCQYSNYPLTFGGGKLEI 238
QY 241 K 241
Db 239 K 239

RESULT 3
US-09-791-537-115236
; Sequence 115236, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115236
; LENGTH: 242
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-115236

Query Match 77.7%; Score 993; DB 5; Length 242;
Best Local Similarity 79.7%; Pred. No. 2.2e-52;
Matches 192; Conservative 18; Mismatches 31; Indels 0; Gaps 0;
QY 1 QVRLQSGGGLVQPGSLRLSCLAAAGTFFDDYAMHWRQAPGKGLWVSGMTWNSGSIGY 60
Db 1 QVQLQESGGGLVQPGSLRFSCLAAAGTFFSNAMNWRQAPGKGLWVSGISGANTYY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTSSG 120

Db 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAKASSLGYYFDYWGQTLVTSSG 120
QY 121 GGGPGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKPGKAPKL 180
Db 121 RGGSGGGGGGSDVMTQSPSFLSAVSGDRITITCRASQGIYNYLAWYQKPGKAPKL 180
QY 181 LIYAASLTQSGVPSRFSFGSGSGTEFTLTISLQPEDFGTYCCQLISYPLTFGGGKVEI 240
Db 181 LIYKASSLASGVPSRFSFGSGSGTDFTLTINSLQPDDEFATYYCQLQSDSYPLTFGGGKVEI 240
QY 241 K 241
Db 241 K 241

RESULT 4
US-09-511-939-2
; Sequence 2, Application US/09511939
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1070
; CURRENT APPLICATION NUMBER: US/09/511,939
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-511-939-2

Query Match 77.6%; Score 992; DB 5; Length 240;
Best Local Similarity 80.6%; Pred. No. 2.6e-52;
Matches 195; Conservative 16; Mismatches 27; Indels 4; Gaps 2;
QY 1 QVRLQSGGGLVQPGSLRLSCLAAAGTFFDDYAMHWRQAPGKGLWVSGMTWNSGSIGY 60
Db 1 EVQLLESGGGLVQPGSLRLSCLAAAGTFFSSYAMSWVRQAPGKGLWVAISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTSSG 120
Db 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAK---SYGAFDYWGQTLVTSSG 117
QY 121 GGGPGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKPGKAPK 179
Db 118 GGGSGGGGGGSDIQMTQSPSSLSASVSDRVITITCRASQSISSYLNWYQKPGKAPK 177
QY 180 LLIYAASLTQSGVPSRFSFGSGSGTEFTLTISLQPEDFGTYCCQLISYPLTFGGGKVEI 239
Db 178 LLIYAASLTQSGVPSRFSFGSGSGTDFTLTISLQPEDFGTYCCQSYSTPNTFQGQTKVEI 237
QY 240 IK 241
Db 238 IK 239

RESULT 5
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M

```
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/031135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match      77.6%; Score 992; DB 5; Length 240;
Best Local Similarity 80.6%; Pred. No. 2.6e-52;
Matches 195; Conservative 16; Mismatches 27; Indels 4; Gaps 2;

QY 1 QVRLQSGGGLVQGRSLRLSCLAAAGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 EVQLLESGGGLVQPGSLRLSCLAAAGFTFESSYAMSWVRQAPGKGLEWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 120
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAK---SYGAFDYWGQGTLLTVTVSSG 117

QY 121 GGGPGGGGGGGS-DVVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKPGKAPK 179
Db 118 GGGGGGGGGGSDIQMTQSPSSLSASVGRVITITCRASQSISSYLNWYQKPGKAPK 177

QY 180 LLIYAASTLQSGVPSRFSGSGGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGTKVE 239
Db 178 LLIYAASSLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQSYSTPNTFQGQTKVE 237

QY 240 IK 241
Db 238 IK 239

RESULT 6
US-09-791-537-121731
; Sequence 121731, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 121731
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-121731
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Query Match      77.5%; Score 991; DB 5; Length 239;
Best Local Similarity 77.6%; Pred. No. 2.9e-52;
Matches 187; Conservative 24; Mismatches 28; Indels 2; Gaps 1;
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QY 1 QVRLQSGGGLVQGRSLRLSCLAAAGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 QVQLVQSGGGLVQPGSLRLSCLAAAGFTLRTYGMHWVRQAPGKGLEWAGISFDGRSEYY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 120
Db 61 ADSVQGRFTISRDSKNTLYLQMNSLRAEDTAVYYCARGAHY--GFDIWGQGTMTVTVSSG 118

QY 121 GGGPGGGGGGSDVVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKPGKAPKL 180
Db 119 GGGTGGGGGGGSDIQMTQSPSTLSASIGDRVITITCRASEGIYHMLAWYQKPGKAPKL 178

QY 181 LIYAASTLQSGVPSRFSGSGGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGGKVEI 240
Db 179 LIYKASSLASGAPSRFSGSGGTDFTLTISLQPDDEFATYYCQQYSNYPLTFGGGKLEI 238

QY 241 K 241
Db 239 K 239

RESULT 7
US-09-791-537-115235
; Sequence 115235, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115235
; LENGTH: 248
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-115235
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Query Match      73.4%; Score 938; DB 5; Length 248;
Best Local Similarity 74.9%; Pred. No. 4.4e-49;
Matches 185; Conservative 20; Mismatches 36; Indels 6; Gaps 2;
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QY 1 QVRLQSGGGLVQGRSLRLSCLAAAGFTFDDYAMHWVRQAPGKGLEWVSGM--TWNSGSI 58
Db 1 QVQLQESGGGLVKPGSLRLSCLAAAGFTFSSYSMNWVRQAPGKLEWVGRIKSKTDGCTT 60

QY 59 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYC---AREPHNTDAFDIWRGTL 114
Db 61 DYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTRMVRGVITGRWFDPWGQGTL 120

QY 115 VTVSSGGGPGGGGGSDVVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKQP 174
Db 121 VTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDVITITCRASQSISSYLNWYQKQP 180

QY 175 GKAPKLLIYAASTLQSGVPSRFSGSGGTEFTLTISLQPEDFGTYTCQQLISYPLTFGG 234
Db 181 GKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISLQPDDEFATYYCQQYNSYWTFGQ 240

QY 235 GTKVEIK 241
Db 241 GTKLEIK 247
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RESULT 8
US-10-127-890-148
; Sequence 148, Application US/10127890
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
```


Db 63 PSLKDKFIISDNDNAKNTLYLQMSKVRSEDTALYYCARRGY--ANDYWGQGTSTVTSSGG 120
QY 122 GPGCGGGGGGGSDVVMTQSPSFLSAFVGDITITICRASQGIYNYLAWYQKPGKAPKLL 181
Db 121 GSGGGGGGGGSDIVMTQSPASLSASVGETVITICRASENIYSYLAWYQKQKSPQLL 180
QY 182 IYAASTLQSGVPSRFSGSGSGTEFTLTISSLOPEDFGTYCQQLISYPLTFGGGKVEIK 241
Db 181 VYNAKTLAEGVPSRFSGSGSGTQPSLKINSLOPEDFGSYVQHHYGTPTFTFGSGTKLEIK 240

RESULT 14
US-09-791-537-128028
; Sequence 128028, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 128028
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-128028

Query Match 68.9%; Score 880; DB 5; Length 232;
Best Local Similarity 70.4%; Pred. No. 1.2e-45;
Matches 174; Conservative 23; Mismatches 28; Indels 22; Gaps 4;

QY 1 QVRLQQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 QVQLVQSGGQVHPGRSLKLSGAGSGFTFSDYDMHWVRQAPGKGLEWVAVM-WFDGTEKY 59
QY 61 -ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPH-----NTDAFDIWRGTL 114
Db 60 SAESVKGRTISRDNKNTLFLQMNLSRADDTAVYYCAREPDWLLWGDRLDVWGQGT 119
QY 115 VTYSGGGGPGGGGGSDVVMTQSPSFLSAFVGDITITICRASQGIYNYLAWYQKQP 174
Db 120 VTVS-----SDIVMTQSPSTLSASVGDRTITICRASQSISWLAWYQKQP 164
QY 175 GKAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLOPEDFGTYCQQLISYPLTFGG 234
Db 165 GKAPKLLMYEASSLESQVPSRFSGSGSGTEFTLTISSLOPDDEFAAYYCQHYNTYPTFGQ 224
QY 235 GPKVEIK 241
Db 225 GPKLEIK 231

RESULT 15
US-09-791-537-22734
; Sequence 22734, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22734
; LENGTH: 244

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-22734
Query Match 68.7%; Score 878; DB 5; Length 244;
Best Local Similarity 66.3%; Pred. No. 1.7e-45;
Matches 161; Conservative 40; Mismatches 40; Indels 2; Gaps 1;
QY 1 QVRLQQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 QVQLVQSGAEVKKPGDSVKVCKASGYTFSDHYMHVVRQAPGQGLEWMGWIDPNNGDTRF 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAF--DIWGRGTLVTVS 118
Db 61 AQRFGGRVTMTTRDTSISAAYMEVSRRLRSDDTAVYYCAREGTGSAIYGMVWVGQGLVTVS 120
QY 119 SGGGPGGGGGGGSDVVMTQSPSFLSAFVGDITITICRASQGIYNYLAWYQKPGKAP 178
Db 121 SGGGSGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHHLAWYQKPGKAP 180
QY 179 KLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLOPEDFGTYCQQLISYPLTFGGGTKV 238
Db 181 KFLIYKASSLASGAPSRFSGSGSGTDFTLTISSLPDDFATYYCQYSNYPLTFGGGTKL 240
QY 239 EIK 241
Db 241 EIK 243

Search completed: August 15, 2002, 16:27:07
Job time: 372 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:22:15 ; Search time 39.61 Seconds
(without alignments)
148.613 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQSGGGLVQPGRLRL.....CQQLISYPLTFGGGKKEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1010.5	79.1	245	4	US-08-918-148-75
2	1002.5	78.4	245	4	US-08-918-148-78
3	987.5	77.3	245	4	US-08-918-148-76
4	987	77.2	244	4	US-08-918-148-77
5	939.5	73.5	284	4	US-08-564-164A-2
6	901.5	70.5	240	1	US-08-488-113B-148
7	901.5	70.5	240	1	US-08-477-484B-148
8	901.5	70.5	240	2	US-08-646-360-148
9	901.5	70.5	240	4	US-08-839-765-148
10	901.5	70.5	240	4	US-09-136-389-148
11	882	69.0	243	1	US-07-958-140-2
12	882	69.0	243	5	PCT-US93-09166-2
13	879	68.8	301	2	US-08-661-052-14
14	879	68.8	301	4	US-09-188-082-14
15	879	68.8	553	2	US-08-661-052-16
16	879	68.8	553	4	US-09-188-082-16
17	873	68.3	248	2	US-08-887-352B-22
18	873	68.3	248	4	US-09-109-207C-22
19	873	68.3	248	4	US-09-296-005-22
20	868.5	68.0	281	4	US-09-025-769B-178
21	864	67.6	248	2	US-08-887-352B-23
22	864	67.6	248	4	US-09-109-207C-23
23	864	67.6	248	4	US-09-296-005-23
24	847.5	66.3	277	2	US-08-256-790-2
25	825	64.6	255	4	US-09-553-498-8
26	817.5	64.0	282	2	US-08-860-174A-10
27	817	63.9	236	2	US-08-190-199A-65

28	808.5	63.3	246	1	US-07-843-125-1	Sequence 1, Appli
29	805	63.0	240	2	US-08-956-047-25	Sequence 25, Appl
30	792.5	62.0	247	4	US-09-227-693-34	Sequence 34, Appl
31	792.5	62.0	248	1	US-08-331-398A-34	Sequence 34, Appl
32	792.5	62.0	248	2	US-08-331-397B-34	Sequence 34, Appl
33	792.5	62.0	248	2	US-08-759-804A-34	Sequence 34, Appl
34	784	61.3	309	4	US-09-079-029-9	Sequence 9, Appli
35	783.5	61.3	310	4	US-09-079-029-11	Sequence 11, Appl
36	783	61.3	269	4	US-08-646-265A-109	Sequence 109, App
37	779.5	61.0	246	1	US-07-843-125-11	Sequence 11, Appl
38	777	60.8	264	4	US-08-564-164A-4	Sequence 4, Appli
39	769.5	60.2	267	4	US-09-485-737B-2	Sequence 2, Appli
40	769.5	60.2	541	4	US-09-485-737B-85	Sequence 85, Appl
41	769.5	60.2	711	4	US-09-485-737B-90	Sequence 90, Appl
42	766	59.9	239	2	US-08-553-497A-18	Sequence 18, Appl
43	762	59.6	637	1	US-08-235-838-14	Sequence 14, Appl
44	762	59.6	637	2	US-08-465-473B-14	Sequence 14, Appl
45	762	59.6	711	1	US-08-235-838-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-75

Query Match	79.1%;	Score 1010.5;	DB 4;	Length 245;
Best Local Similarity	79.3%;	Pred. No. 3.6e-72;		
Matches 191;	Conservative 23;	Mismatches 26;	Indels 1;	Gaps 1;
QY	1	QVRLQSGGGLVQPGRLRLS	CAASGFTFDDYAMHWVRQAPGKGL	EWSGMTWNSGSIGY 60
Db	3	EVQLVQSGGGLVKPGSLRLS	CAASGFTFSDYMSWIRQAPGKGL	EWYSISSGSTIYY 62
QY	61	ADSVKGRFTISRDNKNSLYLQ	MNSLRAEDTAVYYCAREPHNTDA	FDIWGRTLVTVSSG 120
Db	63	ADSVKGRFTISRDNKNTLYLQ	MNSLRAEDTAVYYCARW-SGEDA	FDIWGGQTMVTVSSG 121
QY	121	GGGPGGGGGGGSDVMTQSP	SFSLSAFVGDITITCRASQGIY	NYLAWYQQKPKAPKL 180
Db	122	GGGSGGGGGGGSDIVMTQSP	STLSASVGDRAITCRASEGIY	HWLAWYQQKPKAPKL 181
QY	181	LIYAASTLQSGVPSRFRSGS	GSGTEFTLTSSLOPEDFGTY	YCQQLISYPLTFGGGKVEI 240
Db	182	LIYKASSLASGAPSRFRSGS	GSGADFTLTSSLPDDFATY	YCQYSNYPLTFGGGKLEV 241
QY	241	K 241		
Db	242	K 242		

RESULT 2

US-08-918-148-78
; Sequence 78, Application US/08918148A

;; TITLE OF INVENTION: Thereof
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rhone-Poulenc Rorer Inc.
;; STREET: 500 Arcola Road, 3C43
;; CITY: Collegeville
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19426-0107
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/564,164A
;; FILING DATE: 28-DEC-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/FR94/00714
;; FILING DATE: 15-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 93/07241
;; FILING DATE: 16-JUN-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Savitzky, Martin F.
;; REGISTRATION NUMBER: 29,699
;; REFERENCE/DOCKET NUMBER: ST93030-US
;; TELEPHONE: (610)454-3816
;; TELEFAX: (610)454-3808
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 284 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-564-164A-2

Query Match 73.5%; Score 939.5; DB 4; Length 284;
Best Local Similarity 72.7%; Pred. No. 1.5e-66;
Matches 176; Conservative 29; Mismatches 36; Indels 1; Gaps 1;

Qy 1 QVRLQSGGGLVQGRSLRLSCAASGFTDDYAMHWVROAPGKGLEWVSGMTWNSGSIGY 60
Db 28 QVKLQSGGGLVQGRSLKLSGVSGFTFSNYGMNWIOTPGKGLEWVAYISSGSSLYY 87
Qy 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR-EPHNTDAFDIWRGTLTVSS 119
Db 88 AETVKGRFTISRDNKNTLYLQMTSLRSEDYALYCARHEGTGDTFFDYWGQTTTVSS 147
Qy 120 GGGPGGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKPKAPK 179
Db 148 GGGGGGGGGGGSDVELTQSPHLSASLGETVSIETCLASEGISNYLAWYQKPKSPQ 207
Qy 180 LLIYAASLTQSGVPSRFSGGSGGTEFTLTISLQPEDEFGTYCQQLISYPLTFGGGKVE 239
Db 208 LLIYASLQDGVPSRFSGGSGGTQSLKISNMQPEDEGVYVYQYQAYKYPSTFGAGTKLE 267
Qy 240 IK 241
Db 268 IK 269

RESULT 6
US-08-488-113B-148
; Sequence 148, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,113B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 148:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 240 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-488-113B-148

Query Match 70.5%; Score 901.5; DB 1; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;

Qy 1 QVRLQSGGGLVQGRSLRLSCAASGFTDDYAMHWVROAPGKGLEWVSGMTWNSGSIGY 60
Db 1 ETQLVQSGGGLVKPGSVRISCAASGYTFTNYGMNWRQAPGKLEWMGWINTHTGEPTY 60
Qy 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLTVSSG 120
Db 61 ADSFKGRFTFSLDDSKNTAYLQINSLRAEDTAVYFCTRRGYDW-YFDVWGQGTTVTVSSG 119
Qy 121 GGGPGGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQKPKAPKL 180
Db 120 GGGGGGGGGGGSDIOMTQSPSLSASVGDRTVITCRASQDINSYLSWFFQKPKAPKT 179
Qy 181 LIYAASLTQSGVPSRFSGGSGGTEFTLTISLQPEDEFGTYCQQLISYPLTFGGGKVEI 240
Db 180 LIYRANRLESGVPSRFSGGSGGTDTLTISLQYEDFGIYVYQYQYDESPWTFGGGKLEM 239
Qy 241 K 241

Query Match 70.5%; Score 901.5; DB 2; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;
QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 EIQLVQSGGGLVKPGGSVRISCAASGYFTNYGMNVRQAPGKGLEWGWINTHTGEPTY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTVSSG 120
Db 61 ADSFKGRFTSLDDSKNTAYLQINLSRAEDTAVYFCTRRGYDW-YFDVWGQGTTVTVSSG 119
QY 121 GGGPGGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQQKPGKAPKL 180
Db 120 GGGSGGGGGGGSDIQTQSPSLASVGDRTITCRASQDINSYLSWFOQKPGKAPKT 179
QY 181 LIYAASTLQSGVPSRFSFGSGGTFTLTISLQPEDFGTYCQQLISYPLTFGGGKVEI 240
Db 180 LIYRANRLESGVPSRFSFGSGGTFTLTISLQYEDFGIYCCQYDESPWTFGGGTKLEM 239
QY 241 K 241
Db 240 K 240

RESULT 9
US-08-839-765-148
; Sequence 148, Application US/08839765
; Patent No. 6146531
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-148
Query Match 70.5%; Score 901.5; DB 4; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;
QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 EIQLVQSGGGLVKPGGSVRISCAASGYFTNYGMNVRQAPGKGLEWGWINTHTGEPTY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTVSSG 120
Db 61 ADSFKGRFTSLDDSKNTAYLQINLSRAEDTAVYFCTRRGYDW-YFDVWGQGTTVTVSSG 119
QY 121 GGGPGGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQQKPGKAPKL 180
Db 120 GGGSGGGGGGGSDIQTQSPSLASVGDRTITCRASQDINSYLSWFOQKPGKAPKT 179
QY 181 LIYAASTLQSGVPSRFSFGSGGTFTLTISLQPEDFGTYCQQLISYPLTFGGGKVEI 240
Db 180 LIYRANRLESGVPSRFSFGSGGTFTLTISLQYEDFGIYCCQYDESPWTFGGGTKLEM 239
QY 241 K 241
Db 240 K 240

RESULT 10
US-09-136-389-148
; Sequence 148, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-389-148

Query Match 70.5%; Score 901.5; DB 4; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;

QY 1 QVRLQSGGGLVQPGRLSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSGIGY 60
Db 1 EIQLVQSGGGLVQPGSVRISCAASGYTFTNYGMNWRQAPGKGLEWGMWINTHTGEPTY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTVSSG 120
Db 61 ADSEKGRFTSLDSDNTAYLQINLSRAEDTAVYFCTRRGYDW-YFDVWGQGTITVTVSSG 119
QY 121 GGGPGGGGGGGSDVVMVTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQKPGKAPKL 180
Db 120 GGGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQDINSYLSWFOQKPGKAPKT 179
QY 181 LIYAASTLQSGVPSRFSGSGTGTEFTLTISLQPEDFGTYCYCQQLISYPLTFGGGKVEI 240
Db 180 LIYRANRLESGVPSRFSGSGTDYTLTISLQYEDFGIYYCQYDESPWTFGGGKLEM 239
QY 241 K 241
Db 240 K 240

RESULT 11
US-07-958-140-2
; Sequence 2, Application US/07958140
; Patent No. 5489525
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958.140
; FILING DATE: 19921008
; CLASSIFICATION: 436

; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-958-140-2

Query Match 69.0%; Score 882; DB 1; Length 243;
Best Local Similarity 69.2%; Pred. No. 4.le-62;
Matches 166; Conservative 30; Mismatches 42; Indels 2; Gaps 1;

QY 2 VRLOOSGGGLVQPGRLSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSGIGYA 61
Db 3 VQLVESGGGLVQPGSLKLSCAASGFDPSRYMWSVRQAPGKGLEWIGEINPDSSSTINYT 62
QY 62 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTVSSGG 121
Db 63 PSLKDKFTIISDNRKNTLYLQMSKVRSEDTALYYCARRGY--AMDYWGQGTSTVTVSSGG 120
QY 122 GGPGGGGGGGGSDVVMVTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQKPGKAPKLL 181
Db 121 GSGGGGGGGGGSDIVMTQSPASLSASVGETVITCRASENIYSYLAHYQKQKSPQLL 180
QY 182 IYAASTLQSGVPSRFSGSGTGTEFTLTISLQPEDFGTYCYCQQLISYPLTFGGGKVEIK 241
Db 181 VYNAKTLAEGVPSRFSGSGTGTFSLKINSLOPEDFGSYCYCQHHYGTPTFTFGSGTKLEIK 240

RESULT 12
PCT-US93-09166-2
; Sequence 2, Application PC/TUS9309166
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US93-09166-2

Query Match 69.0%; Score 882; DB 5; Length 243;
Best Local Similarity 69.2%; Pred. No. 4.le-62;
Matches 166; Conservative 30; Mismatches 42; Indels 2; Gaps 1;

QY 2 VRLQSGGGLVQPGRLSLRLSCLASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGSIGYA 61
Db 3 VQLVESGGGLVQPGGSLKLSCLASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGSIGYA 62
QY 62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTDAFDIWRGTLTVSSG 121
Db 63 PSLKDKFISSDNKNTLYLQMSKVRSEDTALYYCARRGYV-AMDYWGQGTSTVTVSSG 120
QY 122 GPGGGGGGGGSDIVMTQSPSLASVGVDTITITCRASQGIYNYLAWYQKPKAKILL 181
Db 121 GSGGGGGGGGSDIVMTQSPSLASVGVDTITITCRASENIYSLAWYQKQKSPOLL 180
QY 182 IYAASTLQSGVPSRFSGGSGTFTLTISLQPEDFGTYTCQQLISYPLTFEGGKVEIK 241
Db 181 VYNAKTLAEGVPSRFSGGSGTFTLTISLQPEDFGTYTCQHHYGTPTFTFGSGTKLEIK 240

RESULT 13
US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-14

Query Match 68.8%; Score 879; DB 2; Length 301;
Best Local Similarity 69.6%; Pred. No. 9e-62;
Matches 172; Conservative 27; Mismatches 40; Indels 8; Gaps 3;

QY 2 VRLQSGGGLVQPGRLSLRLSCLASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGSIGYA 61
Db 21 IQLVESGGGVQPGRLSLRLSCSSGFIISDNYMYWVRQAPGKLEWVATISDGGSYTYYP 80
QY 62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTD-AFDIWRGTLTVSSG 120
Db 81 DSVKGRFTISRDNKNTLFLQMSLRLPEDTGVYFCARGYRYREGAMDYWGQGTPTVTVSSG 140
QY 121 GPGGGGGGGGSDVMTQSPSLASVGVDTITITCRASQGIY-----NYLAWYQKPK 174
Db 141 GSGGGGGGGGSDIQLTQSPSLASVGVDRVTITCKSSQSVLYSSNQKNYLAWYQKPK 200
QY 175 GKAPKLLIYAASTLQSGVPSRFSGGSGTFTLTISLQPEDFGTYTCQQLISYPLTFGG 234
Db 201 GKAPKLLIYAASTLQSGVPSRFSGGSGTFTLTISLQPEDFGTYTCQQLISYPLTFGG 234
QY 235 GTKVEIK 241
Db 260 GTKVEIK 266

RESULT 14
US-09-188-082-14
; Sequence 14, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-14

Query Match 68.8%; Score 879; DB 4; Length 301;
Best Local Similarity 69.6%; Pred. No. 9e-62;
Matches 172; Conservative 27; Mismatches 40; Indels 8; Gaps 3;
QY 2 VRLQSGGGLVQPGRLSLRLSCLASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGSIGYA 61

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:24:04 ; Search time 101.13 Seconds
(without alignments)
264.697 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQSGGGLVQGRSLRL.....COOLISYPLTFGGGTRKEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1278	100.0	241	18 AAW24063	Human WSX receptor
2	1040	81.4	242	21 AAY58236	Internalising anti
3	1023.5	80.1	248	13 AAR20059	Recombinant sc3D6
4	1010.5	79.1	245	20 AAY06714	Antibody 5E5 singl
5	1009.5	79.0	245	20 AAY06717	Antibody 12B5 sing
6	993.5	77.7	293	22 AAG65715	Amino acid sequenc
7	992	77.6	240	20 AAY02472	A single chain ant
8	988	77.3	240	22 AAB46044	Human TF anti-idio
9	988	77.3	240	22 AAB46045	Human TF anti-idio
10	987.5	77.3	245	20 AAY06715	Antibody 10D10 sin
11	987	77.2	244	20 AAY06716	Antibody 12B5 sing

12	985	77.1	240	22 AAB46040	Human TF anti-idio
13	984	77.0	240	22 AAB45992	Human MUC-1 scFv C
14	977	76.4	240	22 AAB46039	Human TF anti-idio
15	977	76.4	240	22 AAB46048	Human TF anti-idio
16	976	76.4	240	22 AAB46010	Human MUC-1 scFv C
17	976	76.4	240	22 AAB46042	Human TF anti-idio
18	975	76.3	240	22 AAB45997	Human MUC-1 scFv C
19	975	76.3	240	22 AAB46007	Human MUC-1 scFv C
20	975	76.3	240	22 AAB46018	Human MUC-1 scFv C
21	975	76.3	240	22 AAB46020	Human MUC-1 scFv C
22	974	76.2	240	22 AAB46050	Human TF anti-idio
23	972	76.1	240	22 AAB46004	Human MUC-1 scFv C
24	972	76.1	240	22 AAB46038	Human TF anti-idio
25	971	76.0	240	22 AAB46051	Human TF anti-idio
26	970	75.9	240	22 AAB45991	Human MUC-1 scFv C
27	970	75.9	240	22 AAB46043	Human TF anti-idio
28	969	75.8	240	22 AAB46005	Human MUC-1 scFv C
29	969	75.8	240	22 AAB46046	Human TF anti-idio
30	968	75.7	240	22 AAB45993	Human MUC-1 scFv C
31	966	75.6	240	22 AAB45996	Human MUC-1 scFv C
32	966	75.6	240	22 AAB46003	Human MUC-1 scFv C
33	966	75.6	240	22 AAB46006	Human MUC-1 scFv C
34	966	75.6	240	22 AAB46047	Human TF anti-idio
35	964	75.4	240	22 AAB46021	Human MUC-1 scFv C
36	962	75.3	240	22 AAB45999	Human MUC-1 scFv C
37	962	75.3	240	22 AAB46002	Human MUC-1 scFv C
38	962	75.3	240	22 AAB46019	Human MUC-1 scFv C
39	961	75.2	240	22 AAB46009	Human MUC-1 scFv C
40	961	75.2	240	22 AAB46041	Human TF anti-idio
41	960	75.1	240	22 AAB46001	Human MUC-1 scFv C
42	959	75.0	240	22 AAB46012	Human MUC-1 scFv C
43	956	74.8	240	22 AAB45994	Human MUC-1 scFv C
44	955	74.7	240	22 AAB46014	Human MUC-1 scFv C
45	954	74.6	240	22 AAB46011	Human MUC-1 scFv C

ALIGNMENTS

RESULT 1
AAW24063
ID AAW24063 standard; Protein; 241 AA.
XX
AC AAW24063;
XX
DT 17-MAR-1998 (first entry)
XX
DE Human WSX receptor agonist antibody clone #17.
XX
KW Human; WSX receptor; clone #17; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.
XX
OS Homo sapiens.
XX
PN WO9725425-A1.
XX
PD 17-JUL-1997.
XX
PF 07-JAN-1997; 97WO-US00325.
XX
PR 20-JUN-1996; 96US-0667197.
PR 08-JAN-1996; 96US-0585005.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX

DR	WPI; 1997-372864/34.	
XX	WSX receptor and related antibodies and ligands - used to develop	
PT	products for diagnosis and therapy, e.g. for improving	
PT	haematopoiesis or for treating tumours	
XX		
PS	Example 14; Pages 122-123; 219pp; English.	
XX		
CC	The present sequence is an agonist antibody clone to the human WSX	
CC	receptor, which can be used to identify and purify ligands and	
CC	activators. An anti-WSX receptor antibody can be used as an agonist	
CC	to activate the WSX receptor, leading to enhanced proliferation or	
CC	differentiation of a cell expressing the WSX receptor. It can also	
CC	be used to decrease body weight and/or fat-depot weight and/or food	
CC	intake in an obese mammal. WSX receptor ligands can be used to	
CC	enhance proliferation or differentiation of lymphoid, myeloid or	
CC	erythroid blood cell lineages. This is useful when a mammal,	
CC	especially a human, is suffering from decreased blood cell levels,	
CC	i.e. anaemia, caused by chemotherapy, radiation therapy or bone	
CC	marrow transplantation therapy. It can also be used to repopulate	
CC	blood cells in a mammal. The products can also be used to treat,	
CC	e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,	
CC	polycystic ovarian disease, cardiovascular diseases,	
CC	osteoarthritis, dermatological disorders, hypertension, insulin	
CC	resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer	
CC	and cholelithiasis.	
XX		
SQ	Sequence 241 AA;	
Query Match 100.0%; Score 1278; DB 18; Length 241;		
Best Local Similarity 100.0%; Pred. No. 1.1e-78;		
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 QVRLQSGGGLVQPGRSRLSLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60	
Db		
QY	1 qvrlqsgggglvqpgrrslrlscaasgftfdyamhwvrqapkgglewsgmtwnsgsigy 60	
Db		
QY	61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 120	
Db		
QY	61 adsvkgrftisrdnaknslslylqmnsraedtavyycarephntdafdiwrgtlvtvssg 120	
Db		
QY	121 GGGPGGGGGGGSDVMTQSPSFLSAFVGDITITICRASQGIYNYLAWYQQKPGKAPKL 180	
Db		
QY	121 gggpgggsgggsgsdvmtqspsflsafigdttititcrasqgiynyawqqkpgkapkl 180	
Db		
QY	181 LIYAASTLQSGVPSRFSGSGGTEFTLTISLQPEDFGTYQCQLISYPLTFGGGKVEI 240	
Db		
QY	181 liyaastlqsgvpsrfsfgsggteftltisllqpedfgtyycqqqlisypitfgggtkvei 240	
Db		
QY	241 K 241	
Db	I	
Db	241 k 241	
RESULT 2		
AAV58236		
ID	AAV58236 standard; Protein; 242 AA.	
XX		
AC	AAV58236;	
XX		
DT	27-MAR-2000 (first entry)	
XX		
DE	Internalising anti-c-erbB-2 receptor antibody scFv C1.	
XX		
KW	Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;	
XX	HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.	
OS	Synthetic.	
OS	Homo sapiens.	
XX		
FH	Key Location/Qualifiers	
FT	Region 31..35	

FT		/note= "Heavy chain variable region (VH) complementarity
FT		determining region 1 (CDR1)"
FT	Misc-difference 37	/note= "Encoded by GTN"
FT	Region	50..66
FT		/note= "VH-CDR2"
FT	Region	99..108
FT		/note= "VH-CDR3"
FT	Region	158..168
FT		/note= "Light chain variable region (VL) complementarity
FT		determining region 1 (CDR1)"
FT	Region	184..190
FT		/note= "VL-CDR2"
FT	Region	223..231
FT		/note= "VL-CDR3"
XX	WO9955367-A1.	
PN		
XX	04-NOV-1999.	
PD		
XX		
PF	23-APR-1999; 99WO-US07395.	
XX		
PR	24-APR-1998; 98US-0082953.	
PR	12-FEB-1999; 99US-0250056.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Marks JD, Poul MA;	
XX		
DR	WPI; 2000-072168/06.	
DR	N-PSDB; AA255615.	
XX		
PT	Novel internalizing antibodies used to treat cancer cells -	
XX		
PS	Claim 3; Page 82; 85pp; English.	
XX		
CC	This sequence represents an internalising humanised antibody,	
CC	scFv C1, which specifically binds to the extracellular domain	
CC	of the c-erbB-2 receptor, the protein product of the HER/neu oncogene.	
CC	The scFv C1 antibody binds to the epitope of the c-erbB-2 receptor that	
CC	is bound by C1 antibodies. On binding the c-erbB-2 receptor, the	
CC	antibody is transported into the cell. The c-erbB-2 receptor is a marker	
CC	protein which is overexpressed by 30-50% of breast carcinomas and other	
CC	adenocarcinomas, and thus provides a useful cell surface marker for	
CC	specifically targeting tumour cells. The antibodies of the invention	
CC	are used as tumour-targeting molecules for diagnosis and treatment. The	
CC	antibodies can be attached to effector molecules. The effector molecules	
CC	may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin;	
CC	radionuclides; ligands such as growth factors; therapeutic agents such	
CC	as vinblastine, vindesine or melphalan; ribozymes; or antisense	
CC	molecules. The antibodies may also be used for in vivo or in vitro	
CC	detection and/or quantitation of the c-erb-2 receptor and thus diagnosis	
CC	and/or localisation of cancers characterised by expression of c-erb-2.	
CC	Although antibodies have previously been used to target tumour cells,	
CC	their success has been limited. The utility of prior art antibodies has	
CC	been hampered by the paucity of tumour specific antibodies, antibody	
CC	immunogenicity, low binding affinity, and poor tumour penetration.	
CC	Immunogenicity could be avoided and toxicity reduced if high affinity	
CC	tumour specific human antibodies were available. However, the production	
CC	of human monoclonal antibodies using conventional hybridoma technology	
CC	has proven difficult. Also, most of the antibodies produced react with	
CC	antigens that are also common to non-malignant cells, which makes them	
CC	unsuitable for use as tumour-targeting molecules. The antibodies of the	
CC	invention overcome these difficulties, as they are targetted to a	
CC	tumour-specific antigen, and avoid the problem of immunogenicity as they	
CC	are human in origin.	
XX		
SQ	Sequence 242 AA;	

Query Match 81.4%; Score 1040; DB 21; Length 242;
Best Local Similarity 83.0%; Pred. No. 1.1e-62;
Matches 200; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

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QY      1 QVRLQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
      ||:|:||||| ||||||| ||| ||||||| ||| :| | |
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QY      61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG 120
      ||||||| |||:||||| ||||||| |||:| | | | |
Db      61 adsvkgrftisrdnskntlylqmnslraedtavyycakm dasgsyfnfwgggtlvtvssg 120

QY      121 GGGPGGGGGGGSDVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKL 180
      ||| |||||||: ||||||| ||| ||||||| ||| |||||||
Db      121 gggsgggsgggsettlqtspslsafvgdrititcraspgirnnylawyqqkpgkapkl 180

QY      181 LIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYVYCOQLISYPLTFGGGKVEI 240
      ||||||| ||||||| ||||||| ||||||| ||||||| |||:| | | | |
Db      181 liyaastlqsgvpsrfsrgsgsgtdftltisslqp edfatyyccqynsyplsfgggtkvei 240

QY      241 K 241
      |
Db      241 k 241

RESULT      3
AAR20059
ID      AAR20059 standard; Protein; 248 AA.
XX
AC      AAR20059;
XX
DT      25-MAR-1992 (first entry)
XX
DE      Recombinant sc3D6 anti-HIV gp160 antibody.
XX
KW      Plasmid pUC3D6LC; PUC3D6HC; human immunodeficiency virus; AIDS;
KW      complementarity determining region.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Region
FT      Location/Qualifiers
FT      2..31
FT      /label= Framework_1_heavy_chain
FT      32..36
FT      /label= CDR_1_heavy_chain
FT      37..50
FT      /label= Framework_2_heavy_chain
FT      51..67
FT      /label= CDR_2_heavy_chain
FT      68..99
FT      /label= Framework_3_heavy_chain
FT      100..116
FT      /label= CDR_3_heavy_chain
FT      117..127
FT      /label= Framework_4_heavy_chain
FT      128..142
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FT      143..165
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FT      166..176
FT      /label= CDR_1_light_chain
FT      177..191
FT      /label= Framework_2_light_chain
FT      192..203
FT      /label= CDR_2_light_chain
FT      204..235
FT      /label= Framework_3_light_chain
FT      236..242
FT      /label= CDR_3_light_chain
FT      243..253
FT      /label= Framework_4_light_chain
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PN      WO9118983-A.
XX
PD      12-DEC-1991.
XX
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PF      28-MAY-1991; 91WO-1000067.
XX
PR      29-MAY-1990; 90AT-0001178.
XX
PA      (JUNG/) JUNGBAUER A.
XX
PI      Felgenhauer M, Himmeler G, Kohl J, Steindl F;
XX
DR      WPI; 1992-007468/01.
DR      N-PSDB; AAQ20068.
XX
PT      Recombinant protein which binds to complex viral antigen and
PT      HIV-1 - contains variable region of antibody derived from 3D6
PT      cell line, used for detecting HIV-1 antigen
XX
PS      Claim 4; Page 31; 52pp; German.
XX
CC      The cell line 3D6 (87110301; Porton Down) produces a MAb of the
CC      IgG1/kappa type that reacts specifically with HIV-1 gp41 and also
CC      weakly cross-reacts with HIV-1 gp120. Gene construct sc3D6 was
CC      engineered using the variable region coding regions of the heavy
CC      and light chains of antibody 3D6, joined by a linker. The
CC      recombinant protein binds to HIV gp160.
CC      See also AAQ20066 and AAQ20067.
XX
SQ      Sequence 248 AA;

Query Match      80.1%; Score 1023.5; DB 13; Length 248;
Best Local Similarity 79.4%; Pred. No. 1.4e-61;
Matches 197; Conservative 20; Mismatches 22; Indels 9; Gaps 2;

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      :|:|:||||| ||||||| ||| ||||||| ||| :| | | | |
Db      2 evqlvesggglvqpgslrlscaasgftfndyamhwvrqapgkglewvsgiswdsssigy 61

Qy      61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR-----EPHNTDAFDIWGRGT 113
      ||||||| ||||||| ||||||| |||:| | | | | |
Db      62 adsvkgrftisrdnaknsllylqmnslraedmalyyccvkgdrdydsrgyftvafdiwgggt 121

Qy      114 LVTVSSGGGPGGGGGSDVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQK 173
      :||||| ||| |||||||: ||||| ||| |||:||||| | :|||||
Db      122 mvtvssggsgggsgggsggsgdiqmtqspstlsasvgdrvtitcrasgsrwlawyqqk 181

Qy      174 PGKAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYVYCOQLISYPLTFG 233
      ||| ||||| ||:||||| ||||||| ||||||| ||| ||||| ||:| |
Db      182 pgkvpklliykasslesgvpsrfsrgsgsgteftltisslqpddfatyyccqynsy--sfg 239

Qy      234 GGTKVEIK 241
      ||||:|
Db      240 pgtkvdik 247

RESULT      4
AAY06714
ID      AAY06714 standard; Protein; 245 AA.
XX
AC      AAY06714;
XX
DT      17-JUN-1999 (first entry)
XX
DE      Antibody 5E5 single chain Fv (scFv) fragment.
XX
KW      Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
KW      megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
KW      bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
KW      myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour;; MuSK; CDR;
KW      neuromuscular; muscular dystrophy; complementarity determining region.
XX
OS      Homo sapiens.
XX
PN      WO9910494-A2.
XX
```

PD 04-MAR-1999.
XX
PF 21-AUG-1998; 98WO-US17364.
XX
PR 25-AUG-1997; 97US-0918148.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Carter PJ, Fendly BM, Gurney AL;
XX
DR WPI; 1999-204666/17.
XX
PT New thrombopoietin receptor agonist antibodies - useful for
PT treating immunological or hematological disorders
XX
PS Disclosure; Fig 1; 86pp; English.
XX
CC The invention relates to an agonist antibody (Ab) which binds to a
CC thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
CC be used in the same way and for the same indications as thrombopoietin
CC (TPO). They can stimulate proliferation, differentiation or growth of
CC megakaryocytes. They may also be able to stimulate megakaryocytes to
CC increase platelet production. They can be used for treating
CC immunological or hematopoietic disorders, especially thrombocytopenia.
CC Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia
CC following chemotherapy or bone marrow transplant) may be effectively
CC treated with the antibody compounds as well as disorders such as
CC disseminated intravascular coagulation (DIC), immune thrombocytopenia,
CC (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia,
CC congenital thrombocytopenia, thrombotic thrombocytopenia and
CC myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for
CC treatment of solid tumours or leukaemia, myeloablative chemotherapy for
CC autologous or allogeneic bone marrow transplant, myelodysplasia,
CC idiopathic aplastic anemia, congenital thrombocytopenia, and immune
CC thrombocytopenia. The antibodies which bind to the MuSK receptor can be
CC used for improving neuromuscular function in a patient, e.g. in muscular
CC dystrophy. The products can also be used for detection and diagnosis. The
CC antibodies have a longer half-life than the natural ligand for the TPO-R.
CC Sequences AAY06713-Y06718 represent single chain Fv (scFv) fragments of
CC various antibodies.
XX
SQ Sequence 245 AA;

Query Match 79.1%; Score 1010.5; DB 20; Length 245;
Best Local Similarity 79.3%; Pred. No. 1e-60;
Matches 191; Conservative 23; Mismatches 26; Indels 1; Gaps 1;
QY 1 QVRLQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 3 evqlvqsggglvlpqgslrlscaasgftfsdymwirqapkglewsvysssgstiyy 62
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG 120
Db 63 adsvkgrftisrdnsksntlylqmnsdraedtaavycarw-sgedafdlwgqgtmvtvssg 121
QY 121 GGGPGGGGGGGSDVVMVTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKL 180
Db 122 gggsgggsgsgsgsdvmtqspstlsasvgrvaitcrasegylhwlawyqqkpgkpl 181
QY 181 LIYAASTLQSGVPSRFSGSGGTEFTLTSSLPQEDFGTYCYCQLISYPLTFGGGKTKVEI 240
Db 182 liykasslasgapsrfsrgsggadftltisslpddfatyccqysnypltfgggklev 241
QY 241 K 241
Db 242 k 242

RESULT 5
AAY06717
ID AAY06717 standard; Protein; 245 AA.
XX

AC AAY06717;
XX
DT 17-JUN-1999 (first entry)
XX
DE Antibody 12B5 single chain Fv (scFv) fragment.
XX
KW Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
KW megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;
KW neuromuscular; muscular dystrophy; complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 208
FT /note= "unspecified"
XX
PN WO9910494-A2.
XX
PD 04-MAR-1999.
XX
PF 21-AUG-1998; 98WO-US17364.
XX
PR 25-AUG-1997; 97US-0918148.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Carter PJ, Fendly BM, Gurney AL;
XX
DR WPI; 1999-204666/17.
XX
PT New thrombopoietin receptor agonist antibodies - useful for
PT treating immunological or hematological disorders
XX
PS Disclosure; Fig 1; 86pp; English.
XX
CC The invention relates to an agonist antibody (Ab) which binds to a
CC thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
CC be used in the same way and for the same indications as thrombopoietin
CC (TPO). They can stimulate proliferation, differentiation or growth of
CC megakaryocytes. They may also be able to stimulate megakaryocytes to
CC increase platelet production. They can be used for treating
CC immunological or hematopoietic disorders, especially thrombocytopenia.
CC Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia
CC following chemotherapy or bone marrow transplant) may be effectively
CC treated with the antibody compounds as well as disorders such as
CC disseminated intravascular coagulation (DIC), immune thrombocytopenia,
CC (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia,
CC congenital thrombocytopenia, thrombotic thrombocytopenia and
CC myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for
CC treatment of solid tumours or leukaemia, myeloablative chemotherapy for
CC autologous or allogeneic bone marrow transplant, myelodysplasia,
CC idiopathic aplastic anemia, congenital thrombocytopenia, and immune
CC thrombocytopenia. The antibodies which bind to the MuSK receptor can be
CC used for improving neuromuscular function in a patient, e.g. in muscular
CC dystrophy. The products can also be used for detection and diagnosis. The
CC antibodies have a longer half-life than the natural ligand for the TPO-R.
CC Sequences AAY06713-Y06718 represent single chain Fv (scFv) fragments of
CC various antibodies.
XX
SQ Sequence 245 AA;

Query Match 79.0%; Score 1009.5; DB 20; Length 245;
Best Local Similarity 79.7%; Pred. No. 1.2e-60;
Matches 192; Conservative 22; Mismatches 26; Indels 1; Gaps 1;
QY 1 QVRLQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 3 qvqlvesggglvlpqgslrlscaasgftfsdymwirqapkglewsvysssgstiyy 62
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG 120

Db 63 adsvkgrftisrdnaknslylqmnslraedtavyyccardrgst-gmdvwgrgtlvtvssg 121
QY 121 GGGPGGGSGGGSDVVMQTQSPSFLSAFVGDITITICRASQGIYNYLAWYQKPGKAPKL 180
Db 122 gggsgggsgggsggdiqmtgspstlsasigdrvtitcrasegiyhwlawyqkpgkapkl 181
QY 181 LIYAASTLQSGVPSRFSFGSGSGTEFTLTITSSLOPEDFGTYTCQQLISYPLTFGGGKVEI 240
Db 182 liykasslasgapsrfsfgsgsgtdftxtlsslqpdddfatyycqysnypltfgggtklei 241
QY 241 k 241
Db 242 k 242

RESULT 6
AAG65715
ID AAG65715 standard; protein; 293 AA.
XX
AC AAG65715;
XX
DT 07-JAN-2002 (first entry)
XX
DE Amino acid sequence of secreted form of scFv 4A.
XX
KW Polymeric immunoglobulin receptor; pIgR; ligand; therapeutic;
KW carcinoma diagnosis; veterinary; scFv 4A.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Peptide 1..22 /note= "PelB leader"
FT Peptide 23..27 /note= "FLAG epitope"
FT Region 28..58 /note= "Heavy chain framework 1"
FT Region 59..62 /note= "CDR1"
FT Region 63..76 /note= "Heavy chain framework 2"
FT Region 77..93 /note= "CDR2"
FT Region 94..125 /note= "Heavy chain framework 3"
FT Region 126..139 /note= "CDR3"
FT Region 140..147 /note= "Heavy chain framework 4"
FT Region 148..162 /note= "linker"
FT Region 163..185 /note= "light chain framework 1"
FT Region 186..196 /note= "CDR1"
FT Region 197..211 /note= "light chain framework 2"
FT Region 212..218 /note= "CDR2"
FT Region 219..250 /note= "light chain framework 3"
FT Region 251..259 /note= "CDR3"
FT Region 260..270 /note= "light chain framework 4"
FT Peptide 274..283 /note= "myc epitope tag"
FT Peptide 288..293 /note= "6 His tag"

XX
PN WO200172846-A2.
XX

PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-US09699.
XX
PR 27-MAR-2000; 2000US-192197P.
PR 27-MAR-2000; 2000US-192198P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Mostov KE, Chapin SJ, Richman-Eisenstat J;
XX
DR WPI; 2001-611619/70.
XX
PT New ligands binding to a specific region of a polymeric immunoglobulin
PT receptor, useful for transporting therapeutic or diagnostic
PT compositions into or across cells expressing pIgR e.g. in drug delivery
PT
XX
PS Disclosure; Fig 5; 102pp; English.
XX
CC The invention provides ligands that bind specifically to a region of an
CC animal cell polymeric immunoglobulin receptor (pIgR). The pIgR cleaves
CC to produce a stalk region remaining attached to the cell and a secretory
CC component existing in the organ of interest in several forms. The ligands
CC do not bind to the stalk or the most abundant form of the secretory
CC component present in the organ under physiological conditions. The
CC ligands are useful for transporting therapeutic or diagnostic
CC compositions into or across cells expressing pIgR, useful to introduce
CC or transport ligands such as antibodies and/or to deliver biologically
CC active components such as proteins, nucleic acids or detectable labels.
CC They are used to deliver therapeutic compositions to mucosal surfaces
CC such as the gastro-intestinal tract, respiratory system etc. in humans.
CC They are also useful to label cells expressing pIgR, e.g. to distinguish
CC epithelial cells from a mixed cell population in pathology studies or to
CC aid in carcinoma diagnosis (since pIgR expression is reduced in
CC carcinomas relative to normal epithelium). They can also be used to
CC deliver veterinary compositions, especially in mammals such as farm,
CC domestic or wild mammals or birds e.g. birds reared for human
CC consumption. The present sequence represents the amino acid sequence
CC of secreted form of scFv 4A.
XX
SQ Sequence 293 AA;

Query Match 77.7%; Score 993.5; DB 22; Length 293;
Best Local Similarity 79.3%; Pred. No. 1.7e-59;
Matches 192; Conservative 19; Mismatches 30; Indels 1; Gaps 1;
QY 1 QVRLQQSGGGLVQPCRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 28 qvqlvqsgggglvqpggslrlscaasgftfssyamswwrqapkgglewvsaisgggstyy 87
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYVCARE-PHNTDAFDIWRGTLVTVSS 119
Db 88 adsvkgrftisrdnsknltlylqmnslraedtavyycarsftvnsygfqhwwggtlvtvss 147
QY 120 GGGPGGGSGGGSDVVMQTQSPSFLSAFVGDITITICRASQGIYNYLAWYQKPGKAPK 179
Db 148 gggsgggsgggsggseivltqspstlsasigdrvtitcrasegiyhwlawyqkpgkapk 207
QY 180 LLIYAASTLQSGVPSRFSFGSGSGTEFTLTITSSLOPEDFGTYTCQQLISYPLTFGGGKVE 239
Db 208 lliykasslasgapsrfsfgsgsgtdftlsslqpdddfatyycqhydstptfagggtkvd 267
QY 240 IK 241
Db 268 ik 269

RESULT 7
AAY02472
ID AAY02472 standard; Protein; 240 AA.
XX

AC	AA02472;	
XX		
DT	15-JUL-1999 (first entry)	
XX		
DE	A single chain antibody (ScFv).	
XX		
KW	Screening; functional polypeptide; ligand; non-functional;	
KW	enrichment; single chain antibody; ScFv.	
XX		
OS	Unidentified.	
XX		
PN	W09920749-A1.	
XX		
PD	29-APR-1999.	
XX		
PF	20-OCT-1998; 98WO-GB03135.	
XX		
PR	21-NOV-1997; 97US-0066729.	
PR	20-OCT-1997; 97GB-0022131.	
PR	13-NOV-1997; 97US-0065428.	
XX		
PA	(MEDI-) MEDICAL RES COUNCIL.	
XX		
PI	Tomlinson I, Winter G;	
XX		
DR	WPI; 1999-288302/24.	
DR	N-PSDB; AAX36070.	
XX		
PT	Screening for functional polypeptides which bind a ligand	
XX		
PS	Disclosure; Fig 2; 67pp; English.	
XX		
CC	The specification describes a method for screening for functional	
CC	polypeptides which bind a ligand. The method comprises contacting a	
CC	repertoire of polypeptides with a generic ligand, and then screening	
CC	selected functional polypeptides with a target ligand. The method	
CC	permits the removal from a chosen repertoire of polypeptides, those	
CC	which are non-functional, e.g. as a result of the introduction of	
CC	frame-shift mutations, stop codons, folding mutants or expression	
CC	mutants which would be or are incapable of binding to any target	
CC	ligand. The method also permits the enrichment of a chosen repertoire	
CC	of polypeptides for those polypeptides which are functional, well folded	
CC	and highly expressed. The polypeptides obtained can be used in	
CC	diagnostic, prophylactic and therapeutic procedures. The present	
CC	sequence represents the single chain antibody (ScFv) that forms the	
CC	basis of a library according to the invention.	
XX		
SQ	Sequence 240 AA;	
Query Match 77.6%; Score 992; DB 20; Length 240;		
Best Local Similarity 80.6%; Pred. No. 1.8e-59;		
Matches 195; Conservative 16; Mismatches 27; Indels 4; Gaps 2;		
QY	1 QVRLQSGGGLVQGRSLRLSCAASGFTEDDYMHWVRQAPGKGLEWVSGMTWNSGSIGY 60	
Db	1 evqllesggglvqpggslrlscaasgftfssyamswwrqpapkgkglewvsaisgsgstyy 60	
QY	61 ADSVKGRFTISRDNKNSLYLQMNLSLRAEDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 120	
Db	61 adsvkgrftisrdnsksntlylqmnsdraedtaavycaak---sygafdywgqgtltvtvssg 117	
QY	121 GGGPGGGGGSGGGS-DVVMQTSPSFLSAFVGDITITICRASQGIYNYLAWYQOKPGKAPK 179	
Db	118 gggsgggsgggsggstldqmtqspsslsasvgrvrtitcrasqsissylnwyyqdkpgkapk 177	
QY	180 LLIYAASTLQGVPSRFSGSGTEFTLTISLQPEDFGTYCCQLISVPLTFGGGKVE 239	
Db	178 lliyaasslqsgvpsrfsgsgsgtdftltisslqpedfatyyccqysstptfsgggtkve 237	
QY	240 IK 241	
Db	238 ik 239	

RESULT	8
AA044	
ID	AA044 standard; Peptide; 240 AA.
XX	
AC	AA044;
XX	
DT	23-MAR-2001 (first entry)
XX	
DE	Human TF anti-idiotypic antibody fragment K3.
XX	
KW	MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
KW	antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;
KW	antiparasitic; infectious disease.
XX	
OS	Homo sapiens.
XX	
PN	W0200073430-A2.
XX	
PD	07-DEC-2000.
XX	
PF	29-MAY-2000; 2000WO-DE01809.
XX	
PR	27-MAY-1999; 99DE-1024405.
PR	09-SEP-1999; 99DE-1043016.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Goletz S, Karsten U;
XX	
DR	WPI; 2001-049937/06.
XX	
PT	Vaccines against conformation-dependent or non-peptide antigens, based
PT	on DNA encoding peptide which mimics the antigen, useful e.g. as
PT	antitumor vaccines -
XX	
PS	Disclosure; Page 11; 36pp; German.
XX	
CC	This invention describes a novel vaccine (V1) against
CC	conformation-dependent antigens (CDA) comprising DNA (I) and/or an
CC	antibody, or peptide which immunologically imitates CDA, is new. (I)
CC	encodes a region of an antidiotypic antibody (Ab2) or another peptide
CC	which: (a) specifically binds to the binding site of an antibody (Ab1)
CC	or an antigen binding molecule; and (b) immunologically mimics the
CC	initial antigen. The epitope is partially or completely
CC	conformation-dependent, and has an immunogenic structure defined by a
CC	specific spatial conformation of amino acids. (I) is used in the form
CC	of linear or circular naked DNA and/or with a viral vector and/or
CC	adjuvants. The products of the invention have cytostatic, virucidal,
CC	antibacterial and antiparasitic. The invention also describes (1) a
CC	corresponding vaccine (V2) against antigens which are not proteins or
CC	peptides, as defined above but which have epitopes which show an
CC	immunogenic structure; (2) preparing (V1) and (V2); (3) human
CC	antidiotypic antibody fragments against the MUC1-conformation epitope
CC	having one of 31 approximately 60 residue amino acids sequences, all
CC	fully defined in the specification; (4) MUC1-conformation epitope mimics
CC	having one of 16 9-17 residue amino acid sequences, all fully in the
CC	specification; (5) antidiotypic antibody fragments against the TF
CC	antigen having one of 24 approximately 200 residue amino acid sequences,
CC	fully defined in the specification; (6) TF carbohydrate epitope mimetics
CC	having one of 25 7-13 residue amino acid sequences, all fully defined in
CC	the specification; and (7) DNA sequences encoding the fragments and
CC	derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
CC	cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
CC	and parasites. The vaccines are effective in cases where vaccination has
CC	previously not been possible.
XX	
SQ	Sequence 240 AA;
Query Match 77.3%; Score 988; DB 22; Length 240;	
Best Local Similarity 79.8%; Pred. No. 3.3e-59;	


```
XX DR WPI; 1999-204666/17.
XX
XX PT New thrombopoietin receptor agonist antibodies - useful for
XX PT treating immunological or hematological disorders
XX
XX PS Disclosure; Fig 1; 86pp; English.
XX
XX CC The invention relates to an agonist antibody (Ab) which binds to a
XX CC thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
XX CC be used in the same way and for the same indications as thrombopoietin
XX CC (TPO). They can stimulate proliferation, differentiation or growth of
XX CC megakaryocytes. They may also be able to stimulate megakaryocytes to
XX CC increase platelet production. They can be used for treating
XX CC immunological or hematopoietic disorders, especially thrombocytopenia.
XX CC Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia
XX CC following chemotherapy or bone marrow transplant) may be effectively
XX CC treated with the antibody compounds as well as disorders such as
XX CC disseminated intravascular coagulation (DIC), immune thrombocytopenia,
XX CC (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia,
XX CC congenital thrombocytopenia, thrombotic thrombocytopenia and
XX CC myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for
XX CC treatment of solid tumours or leukaemia, myeloablative chemotherapy for
XX CC autologous or allogeneic bone marrow transplant, myelodysplasia,
XX CC idiopathic aplastic anemia, congenital thrombocytopenia, and immune
XX CC thrombocytopenia. The antibodies which bind to the MuSK receptor can be
XX CC used for improving neuromuscular function in a patient, e.g. in muscular
XX CC dystrophy. The products can also be used for detection and diagnosis. The
XX CC antibodies have a longer half-life than the natural ligand for the TPO-R.
XX CC Sequences AAY06713-Y06718 represent single chain Fv (scFv) fragments of
XX CC various antibodies.
XX
XX SQ Sequence 245 AA;

Query Match 77.3%; Score 987.5; DB 20; Length 245;
Best Local Similarity 77.1%; Pred. No. 3.7e-59;
Matches 185; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 1 QVRLQSGGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 3 evqlvqsgggvqpqgslslscavsgitlrtygmhvwvrqapgkglewagisfdgrseyy 62

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWRGTLVTVSSG 120
Db 63 adsvkggrftisrdnsknltlylqmnsdraedtavyycard-rgsygmdivrgtmvtvssg 121

QY 121 GGGPGGGGGGGSDVVMVTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQOKPGKAPKL 180
Db 122 gggsgggsgggsgsdigmtqspstlsasigdrvtitcrasegiyhwlwagqkpgkapkl 181

QY 181 LIYAASTLQSGVPSRFSGSGGTEFTLTISSLPQEDFGTYTCQQLISYPLTFGGGTKVEI 240
Db 182 liykasslasgaprfsfsgsgtdftltlsslpddfatyycqqysnypltfgggtklei 241

RESULT 11
AAY06716
ID AAY06716 standard; Protein; 244 AA.
XX
XX AC AAY06716;
XX
XX DT 17-JUN-1999 (first entry)
XX
XX DE Antibody 12B5 single chain Fv (scFv) fragment.
XX
XX KW Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
XX KW megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
XX KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
XX KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;
XX KW neuromuscular; muscular dystrophy; complementarity determining region.
XX
XX OS Homo sapiens.
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XX PN WO9910494-A2.
XX
XX PD 04-MAR-1999.
XX
XX PF 21-AUG-1998; 98WO-US17364.
XX
XX PR 25-AUG-1997; 97US-0918148.
XX
XX (GETH ) GENENTECH INC.
XX
XX PI Adams CW, Carter PJ, Fendly BM, Gurney AL;
XX WPI; 1999-204666/17.
XX
XX PT New thrombopoietin receptor agonist antibodies - useful for
XX PT treating immunological or hematological disorders
XX
XX PS Disclosure; Fig 1; 86pp; English.
XX
XX CC The invention relates to an agonist antibody (Ab) which binds to a
XX CC thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
XX CC be used in the same way and for the same indications as thrombopoietin
XX CC (TPO). They can stimulate proliferation, differentiation or growth of
XX CC megakaryocytes. They may also be able to stimulate megakaryocytes to
XX CC increase platelet production. They can be used for treating
XX CC immunological or hematopoietic disorders, especially thrombocytopenia.
XX CC Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia
XX CC following chemotherapy or bone marrow transplant) may be effectively
XX CC treated with the antibody compounds as well as disorders such as
XX CC disseminated intravascular coagulation (DIC), immune thrombocytopenia,
XX CC (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia,
XX CC congenital thrombocytopenia, thrombotic thrombocytopenia and
XX CC myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for
XX CC treatment of solid tumours or leukaemia, myeloablative chemotherapy for
XX CC autologous or allogeneic bone marrow transplant, myelodysplasia,
XX CC idiopathic aplastic anemia, congenital thrombocytopenia, and immune
XX CC thrombocytopenia. The antibodies which bind to the MuSK receptor can be
XX CC used for improving neuromuscular function in a patient, e.g. in muscular
XX CC dystrophy. The products can also be used for detection and diagnosis. The
XX CC antibodies have a longer half-life than the natural ligand for the TPO-R.
XX CC Sequences AAY06713-Y06718 represent single chain Fv (scFv) fragments of
XX CC various antibodies.
XX
XX SQ Sequence 244 AA;

Query Match 77.2%; Score 987; DB 20; Length 244;
Best Local Similarity 77.2%; Pred. No. 3.9e-59;
Matches 186; Conservative 25; Mismatches 28; Indels 2; Gaps 1;

QY 1 QVRLQSGGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 3 qvqlvqsgggglvrpggslslscavsgitlrtygmhvwvrqapgkglewagisfdgrseyy 62

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWRGTLVTVSSG 120
Db 63 adsvkggrftisrdsknltlylqmnsdraedtavyycargahy--gfdlwgggtmvtvssg 120

QY 121 GGGPGGGGGGGSDVVMVTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQOKPGKAPKL 180
Db 121 ggggtggsgggsgsdigmtqspstlsasigdrvtitcrasegiyhwlwagqkpgkapkl 180

QY 181 LIYAASTLQSGVPSRFSGSGGTEFTLTISSLPQEDFGTYTCQQLISYPLTFGGGTKVEI 240
Db 181 liykasslasgaprfsfsgsgtdftltlsslpddfatyycqqysnypltfgggtlelel 240

QY 241 K 241
Db 241 k 241

RESULT 12
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:35:37 ; Search time 91.6 Seconds
(without alignments)
455.150 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQSGGGLVQGRSLRL.....CQQLISYPLTFGGGTVKVEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:	562222
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 s
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Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*
```

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	871.5	68.2	298	11	Q9QYF0	Q9qyf0	mus musculu
2	728	57.0	241	11	Q921A6	Q921a6	mus musculu
3	589.5	46.1	218	11	Q925S1	Q925s1	mus musculu
4	490.5	38.4	112	4	Q9HCC1	Q9hcc1	homo sapien
5	478	37.4	121	4	Q9UL71	Q9ul71	homo sapien
6	468	36.6	597	4	Q96BB9	Q96bb9	homo sapien
7	467.5	36.6	118	4	Q9UL91	Q9ul91	homo sapien
8	452	35.4	108	4	Q9UL79	Q9ul79	homo sapien
9	451	35.3	104	4	Q9UL87	Q9ul87	homo sapien
10	450.5	35.3	107	4	Q96SA9	Q96sa9	homo sapien
11	449	35.1	108	4	Q9UL70	Q9ul70	homo sapien
12	446	34.9	113	4	Q9UL90	Q9ul90	homo sapien
13	440	34.4	108	4	Q9UL77	Q9ul77	homo sapien
14	440	34.4	116	4	Q9UL93	Q9ul93	homo sapien
15	439.5	34.4	494	4	Q96K68	Q96k68	homo sapien
16	435.5	34.1	118	4	Q9UL72	Q9ul72	homo sapien

17	433.5	33.9	473	11	Q91205	Q91205 mus musculus
18	432.5	33.8	122	4	Q9UL84	Q9UL84 homo sapien
19	426.5	33.4	147	4	Q9Y509	Q9Y509 homo sapien
20	424.5	33.2	107	4	Q9UL81	Q9UL81 homo sapien
21	414	32.4	109	11	Q920E6	Q920E6 mus musculus
22	403	31.5	479	11	Q91WP5	Q91wp5 mus musculus
23	401.5	31.4	487	11	Q99KA4	Q99ka4 mus musculus
24	392	30.7	119	11	Q920E7	Q920e7 mus musculus
25	390	30.5	95	4	Q9ULB6	Q9ulb6 homo sapien
26	384	30.0	211	11	Q91XL0	Q91xl0 mus musculus
27	381.5	29.9	109	4	Q9UL85	Q9UL85 homo sapien
28	381.5	29.9	437	11	Q9RIA4	Q9ria4 mus musculus
29	381	29.8	116	4	Q96PF6	Q96pf6 homo sapien
30	379	29.7	108	4	Q9UL83	Q9UL83 homo sapien
31	378	29.6	486	11	Q91Z07	Q91z07 mus musculus
32	377.5	29.5	109	4	Q9UL78	Q9UL78 homo sapien
33	377	29.5	233	11	Q91WS9	Q91ws9 mus musculus
34	375	29.3	131	4	Q9UL88	Q9UL88 homo sapien
35	366	28.6	112	4	Q9UGP3	Q9ugp3 homo sapien
36	364	28.5	480	11	Q91XE1	Q91xel mus musculus
37	363	28.4	214	11	Q9RIA5	Q9ria5 mus musculus
38	361	28.2	170	11	Q925S2	Q925s2 mus musculus
39	357	27.9	111	11	Q920E9	Q920e9 mus musculus
40	356.5	27.9	109	4	Q9UL86	Q9ul86 homo sapien
41	356	27.9	107	11	Q9JL84	Q9jl84 mus musculus
42	354	27.7	473	11	Q9D8L4	Q9d8l4 mus musculus
43	353	27.6	125	4	Q9UL95	Q9ul95 homo sapien
44	351.5	27.5	124	6	Q9N0W6	Q9n0w6 oryctolagus
45	350	27.4	234	11	Q91WF8	Q91wf8 mus musculus

ALIGNMENTS

RESULT	1
Q9QYF0	
ID	Q9QYF0
AC	Q9QYF0; PRELIMINARY; PRT; 298 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	CN 8 SCFV.

Query Match	68.28;	Score 871.5;	DB 11;	Length 298;
Best Local Similarity	68.28;	Pred. No. 4.6e-66;		
Matches 165: Conservative	33;	Mismatches 41;	Indels 3;	Gaps 2;

QY 1 QVRLQQSGGGLVQPGRSLRISCAASGFTFDDYAMHWVRQAPCKGLEWVSGMTWNSGSIGY 60

DB 40 OVKLOOSGGGLVKPGGSIKLSCAASGDSFSRYTMSWVRQAPCKGLEWIGEINPDSSITNY 99


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ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 35.1%; Score 449; DB 4; Length 108;
Best Local Similarity 82.2%; Pred. No. 8.2e-31;
Matches 88; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 135 DVVMTQSPSELSAFVGDITITCRASQGIYNYLAWYQKPGKAPKLLIYAASTLQSGVPS 194
Db 1 DIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQKPGKVPKPSLIYAASTLQSGVPS 60

QY 195 RFGSGSGTFTLTISLQPEDFGTYTCQQLISYPLTFGGGKVEIK 241
Db 61 RFGSGSGTFTLTISLQPEDVATYTCQKYNAPRTFGPGTKLEIK 107

RESULT 12
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
```

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Query Match 34.9%; Score 446; DB 4; Length 113;
Best Local Similarity 71.4%; Pred. No. 1.6e-30;
Matches 85; Conservative 15; Mismatches 13; Indels 6; Gaps 1;

QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTEDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLEWAFIRYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLVTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKD-----LNYWGQGTLTVTSS 113

RESULT 13
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 34.4%; Score 440; DB 4; Length 108;
Best Local Similarity 81.3%; Pred. No. 4.7e-30;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 135 DVVMTQSPSELSAFVGDITITCRASQGIYNYLAWYQKPGKAPKLLIYAASTLQSGVPS 194
Db 1 DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQKPGKAPNLLIYAASSLQSGVPS 60

QY 195 RFGSGSGTFTLTISLQPEDFGTYTCQQLISYPLTFGGGKVEIK 241
Db 61 RFGSGSGTFTLTISLQPEDFATYTCQOSYSTSWTFEGTKVEIK 107

RESULT 14
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RESULT 5
HV3I_HUMAN
ID HV3I_HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
chymotryptic peptides of the H-chain, alignment of the tryptic
peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
PROTEIN.
CC PIR; A02053; G1HUNI.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 119 119
FT SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;

Query Match 34.4%; Score 439; DB 1; Length 119;
Best Local Similarity 71.4%; Pred. No. 1.2e-28;
Matches 85; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVRLQQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLVWVSGMTWNSGSIGY 60
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 1 QVQLVQSGGQVQPGKSLRLSCAASGFTFSRYTIHWVRQAPGKGLVWVAVMSYBGBKHY 60

QY 61 ADSYKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWRGTLVTSS 119
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 ADSVNGRFTISRDSKNTLYLNMSLRLPEDTAVYYCARIRDTFAMFFAHWGQTLVTSS 119

RESULT 6
KV1G_HUMAN
ID KV1G_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
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RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
(macroglubulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR; A01867; K1HUGL.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 34.3%; Score 438; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.3e-28;
Matches 87; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQOKPGKAPKLLIYAASTLQSGVPS 194
|:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 1 DIQMTQSPSSLSASVGDRVTIICRASQIRNDLTWYQOKPGKAPKELIYAASNLSQSGVPS 60

QY 195 RFGSGSGSTEFTLTISLQPEDFGTYCQQLISYPLTFGGGKVEIK 241
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 RFGSGSGAGTEFTLTISLQPEDFATYICLQNSYPRSFQGGKVEIK 107

RESULT 7
KV1S_HUMAN
ID KV1S_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
high-pressure liquid chromatography. The primary structure of a
monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01877; K1HWS.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 40 49
FT SEQUENCE 49 AA; 5500 MW; C1AD3CB0F600FF73 CRC64;
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FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 34.2%; Score 437; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 1.6e-28;
Matches 84; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDTITITCRASQGIYNLAWYQKPGKAPKLLIYAASSTLQSGVPS 194
Db 1 DIQMTQSPSSVSASVGDRTVTITCRASQDISHLAWYQKSGKAPKLLIYSASSLENGVPS 60

QY 195 RFGSGSGTEFTLTISLQPEDFGTYVCQQLISYPLTFGGGKVEIK 241
Db 61 RFGSGSGTEFTLTISLQPEDFATYFCQAHSVPLTFGGGTVDIK 107

RESULT 8
KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHUWE.
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 34.0%; Score 434; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 2.8e-28;
Matches 84; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDTITITCRASQGIYNLAWYQKPGKAPKLLIYAASSTLQSGVPS 194
Db 1 DIQMTQSPSSLSASVGDRTVTITCRASQGIKNDLWYQKPGTAPKRLIYGATSLQSGVPS 60

QY 195 RFGSGSGTEFTLTISLQPEDFGTYVCQQLISYPLTFGGGKVEIK 241
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Db 61 RFGSGSGTEFTLTINSLQPEDFATYYCLOYSFPWTFGQGTKEVK 107

RESULT 9
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC PIR; A01883; KIHUWK.
CC HSSP; P01607; IREI.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 33.9%; Score 433; DB 1; Length 129;
Best Local Similarity 77.5%; Pred. No. 4.1e-28;
Matches 86; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 131 GCGSDVVMVTQSPSFLSAFVGDTITITCRASQGIYNLAWYQKPGKAPKLLIYAASSTLQ 190
Db 19 GARCIDIQMTQSPSLSASVGDRTVTITCRASQSIISNLYNWYQKPGKAPKLLIYAASSTLQ 78

QY 191 GVPSPRFGSGSGTEFTLTISLQPEDFGTYVCQQLISYPLTFGGGKVEIK 241
Db 79 GVTSPRFGSGSGTEFTLTISLQPEDSATYYCQQSISTLTITFGQGTREIK 129

RESULT 10
KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```



```
Query Match      33.3%; Score 426; DB 1; Length 108;
Best Local Similarity 74.8%; Pred. No. 1.2e-27;
Matches 80; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDTITITCRASQGIYVLAHYQKPGKAPKLLIYAASTLQSGVPS 194
   I: ||||| ||| ||| :||||| ||| : |||: |||: |||: ||| ||| |||: |||
Db 1 DIQMTQSPSSLSASVGDRTVTITCRASQDITNIVNMFQQRPGQAPKVLIGASILETGVP 60

QY 195 RFGSGSGTEFTLTISLQPEDFGTYCYQQLISYPLTFGGGKVEIK 241
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 RFGSGSGTEFTLTISLQPEDIATYCYQDYDTLPLTFGGGKVDIK 107

RESULT 13
HV3H_HUMAN
ID HV3H_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human Igm immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A02052; M3HUGA.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 122 122
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match      33.2%; Score 424.5; DB 1; Length 122;
Best Local Similarity 64.8%; Pred. No. 1.8e-27;
Matches 79; Conservative 19; Mismatches 21; Indels 3; Gaps 1;

QY 1 QVRLQSGGGLVQGRSLRLSCAASGTFDDBYAMHWVRQAPGKGLVWSGTMNSGSIGY 60
   ||| :||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 QVZLVZSGGAVZPGRSLRLSCAASGFSFSTYAMHWVRQAPGKGLZWLVSISYBGBZYY 60

QY 61 ADSVKGRFTTISRDNKNSLYLQMNLSRAEDTAVYYCAREP---HNTDAFDIWRGTLTV 117
   | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AASVKGRFTTISRDBSKBTMYLEMNSLRAENTAVYYCARGIALGVSAGTDYWGZGLVTI 120

QY 118 SS 119
   ||
Db 121 SS 122

RESULT 14
KV1X_HUMAN
ID KV1X_HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00966; CAA25478.1; ALT_TERM.
DR PIR; A01884; KIHUDI.
DR HSSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 22
FT CHAIN / 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Query Match      33.0%; Score 422; DB 1; Length 129;
Best Local Similarity 75.7%; Pred. No. 3.1e-27;
Matches 81; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDTITITCRASQGIYVLAHYQKPGKAPKLLIYAASTLQSGVPS 194
   I: ||||| ||| ||| :||||| ||| : |||: |||: |||: ||| ||| |||: |||
Db 23 DIQMTQSPSSLSASVGDRTVTITCRAGHNTNPLSWYQKPGKAPTLLIYAVSNLQVGVPS 82

QY 195 RFGSGSGTEFTLTISLQPEDFGTYCYQQLISYPLTFGGGKVEIK 241
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 RFGSGSGAEFTLTISLQPEDFATYCYQNYNFSFTFGGKTKVDNK 129

RESULT 15
KVIL_HUMAN
ID KVIL_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeidler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
RT sequence of the variable part of a human L-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
```

CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01870; K1HUKU.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Benice-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match 32.9%; Score 420; DB 1; Length 108;
Best Local Similarity 75.7%; Pred. No. 3.6e-27;
Matches 81; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQOKPGKAPKLLIYAASTLQSGVPS 194
Db 1 DIQMTQSPSTQPASVGDRTITCRASQSINIWLAWYQOKPEKAPKLLIYKASTLETGVP 60

QY 195 RPSGSGSGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGGKVEIK 241
Db 61 RPSGSGSGTEFTLTINSIQDDFATYTCQYSRYPTFGGQTKLDIK 107

Search completed: August 15, 2002, 16:36:10
Job time: 720 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:25:02 ; Search time 54.95 Seconds
(without alignments)
421.429 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQSGGGLVQPGRSRL.....CQQLISYPLTFGGTKVEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	704.5	55.1	249	2 S41374	single chain Fv an
2	697	54.5	268	2 A56446	Ig heavy chain V r
3	631.5	49.4	233	2 JC5322	p53 specific singl
4	562.5	44.0	128	2 S31595	Ig heavy chain V r
5	552	43.2	121	2 S31118	Ig heavy chain - h
6	543	42.5	121	2 S31104	Ig heavy chain (su
7	543	42.5	123	2 S30532	Ig heavy chain V r
8	527	41.2	120	2 S36273	Ig heavy chain V r
9	518.5	40.6	145	2 S11239	Ig heavy chain V r
10	498	39.0	119	2 F36005	Ig heavy chain V r
11	489	38.3	98	2 S26927	Ig heavy chain V r
12	487	38.1	123	2 PC4281	anti-SS-A/Ro 60k p
13	487	38.1	132	2 S40334	Ig kappa chain - h
14	482	37.7	119	2 S31107	Ig heavy chain - h
15	482	37.7	119	2 S31108	Ig heavy chain - h
16	480.5	37.6	141	2 S31669	Ig heavy chain V r
17	480	37.6	119	2 D36005	Ig heavy chain V r
18	479.5	37.5	137	2 S31701	Ig heavy chain V r
19	478.5	37.4	112	2 PH1654	Ig heavy chain V r
20	478.5	37.4	122	2 E36005	Ig heavy chain V r
21	478	37.4	108	2 S36279	Ig lambda chain V
22	478	37.4	120	2 S36278	Ig heavy chain V r
23	477.5	37.4	120	2 S44111	Ig heavy chain V-D
24	477.5	37.4	122	2 S31117	Ig heavy chain - h
25	476	37.2	108	2 S36277	Ig lambda chain V
26	475.5	37.2	124	2 S40336	Ig kappa chain V-J
27	475	37.2	138	2 S31666	Ig heavy chain V r
28	474	37.1	119	2 C36005	Ig heavy chain V r
29	473.5	37.1	118	2 S31105	Ig heavy chain (su

ALIGNMENTS

RESULT 1

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsaenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti
A:Reference number: S41374
A:Accession: S41374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 55.1%; Score 704.5; DB 2; Length 249;
Best Local Similarity 53.7%; Pred. No. 3.4e-44;
Matches 132; Conservative 43; Mismatches 66; Indels 5; Gaps 1;

QY	1	QVRLQSGGGLVQPGRSRLSCAASGFTFDDYAMHWVRQAPGKGLVWVGMTWNSGSIGY	60
Db	1	QVQLQQSGAELVRPGASVKLSCTASGTFKDDYIHWVKRPEKGLEWIAIPASGNVKY	60
QY	61	ADSVKGRFTISRDNAKNSLYLQMSLRRAEDTAVYVCAREPHNTDAFDIWRGRLTVTVSSG	120
Db	61	VPRFQDKATITADTSSNTAYLLLSLTSEDTAVYVCARRDTLYTSLGYWGQGSTVTVSSR	120
QY	121	GGGPGGGGGGGSDVMTQSPSFLSAFVGDITITCRASQGIY-----NYLAWYQQKPG	175
Db	121	GGGSGGGGGGGSDIELTQSPSPVIVPGESVSISSRSKSLLSYSDGDSYLFWFLQRP	180
QY	176	KAPKLLIYAASLTQSGVPSRFRSGSGSGTEFTLTISSLQPEDFGTYTCQQLISYPLTFGGG	235
Db	181	QSPQLLIYRMSNLASGVDPDRFSGSGSGTSFTLRISRVEAEDVGVYCMQHREYPLTFGAG	240
QY	236	TKVEIK 241	
Db	241	TKLELK 246	

RESULT 2

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide
A:Reference number: A56446; MUID:95229583

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S31104
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633
A:Accession: S31104
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <RAA>
A:Cross-references: EMBL:X63080; NID:g32646; PIDN:CAA44802.1; PID:g32647
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.5%; Score 543; DB 2; Length 121;
Best Local Similarity 85.1%; Pred. No. 8.2e-33;
Matches 103; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

QY 1 QVRLQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
:|:| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDA--FDIWRGRTLTVTS 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAKDVFGSWGWFDLWGRGRTLTVTS 120
QY 119 S 119
|
Db 121 S 121

RESULT 7
S30532
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C:Accession: S30532
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MAR>
A:Cross-references: EMBL:Z18318
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.5%; Score 543; DB 2; Length 123;
Best Local Similarity 82.1%; Pred. No. 8.4e-33;
Matches 101; Conservative 16; Mismatches 2; Indels 4; Gaps 2;

QY 1 QVRLQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
:|:| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGTLGY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARE-PHN---TDAFDIWRGRTLVT 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFAISRDNKNSLYLQMNSLRAEDTALYYCAKDTPTYSSGSWNAFDIWGGQTMVT 120
QY 117 VSS 119
|||
Db 121 VSS 123

RESULT 8
S36273
Ig heavy chain V region (clone alpha-THY-32) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36273
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries
A:Reference number: S36256; MUID:93178448
A:Accession: S36273
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-120 <GRI>
A:Cross-references: EMBL:Z18834; NID:g33116; PIDN:CAA79286.1; PID:g939896
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.2%; Score 527; DB 2; Length 120;
Best Local Similarity 86.7%; Pred. No. 1.2e-31;
Matches 104; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVRLQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
:|:| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISNSGSIGY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDA--FDIWRGRTLTVTS 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCARGIAVAGAYFYDWGQGTTLTVTS 120

RESULT 9
S11239
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S11239
R:Felgenhauer, M.; Kohl, J.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains
A:Reference number: S11239; MUID:90370490
A:Accession: S11239
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <FEL>
A:Cross-references: EMBL:X53613; NID:g23865; PIDN:CAA37675.1; PID:g762936
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.6%; Score 518.5; DB 2; Length 145;
Best Local Similarity 78.6%; Pred. No. 6e-31;
Matches 99; Conservative 12; Mismatches 8; Indels 7; Gaps 1;

QY 1 QVRLQSGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
:|:| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVESGGGLVQPGRSRLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGY 79
QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR-----EPHNTDAFDIWRGT 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVKGRFTISRDNKNSLYLQMNSLRAEDMALYYCVKGRDYDSSGGYFTVAFDIWQGT 139
QY 114 LVTVSS 119
:|||||
Db 140 MVTVSS 145

RESULT 10
F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: F36005

R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571
A:Accession: F36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34026
C:Genetics:
A:Gene: GDB:IGH; IGHDY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 498; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.5e-29;
Matches 93; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVRLOQSGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
II:I :||||:|||||:|||||:|||||:|||||:|||||: :||
Db 1 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWRGTLTVSS 119
|||||:|||||:|||||:|||||:|||||:|||||: :|||||:|||||
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARDRKASDAFDIWRGTLTVSS 119

RESULT 11
S26927
Ig heavy chain V region (DP-31) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26927
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117
A:Accession: S26927
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12333; NID:g32885; PIDN:CAA78203.1; PID:g32886
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 489; DB 2; Length 98;
Best Local Similarity 91.8%; Pred. No. 5.4e-29;
Matches 90; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVRLOQSGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
:|:| :||||:|||||:|||||:|||||:|||||:|||||: :|||||
Db 1 EVQLVESGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 98
|||||:|||||:|||||:|||||:|||||:|||||: :|||||
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAK 98

RESULT 12
PC4281
anti-SS-A/Ro 60K peptide heavy chain E-56 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C:Accession: PC4281
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A:Title: Molecular-cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin

A:Reference number: PC4279; MUID:97236289
A:Accession: PC4281
A:Molecule type: protein
A:Residues: 1-123 <SUZ>
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sj
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 38.1%; Score 487; DB 2; Length 123;
Best Local Similarity 74.6%; Pred. No. 9.7e-29;
Matches 91; Conservative 15; Mismatches 12; Indels 4; Gaps 1;

QY 1 QVRLOQSGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
:|:| :||||:|||||:|||||:|||||:|||||:|||||: :|||||
Db 1 EVQLLESGGGLVQPGRSRLRLSCTVSGFTIGDYAMSWVRQAPGKGLEWVSSISWNSGTIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARE---PHNTDAFDIWRGTLVT 116
|||||:|||||:|||||:|||||:|||||:|||||: :|||:|||||
Db 61 MDSVKGRFTISRDNKNSLYLQMNSLRPEDTALYYCAKDRSDSGYDSRFDIWGGQTAVT 120

QY 117 VS 118
||
Db 121 VS 122

RESULT 13
S40334
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40334
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 38.1%; Score 487; DB 2; Length 132;
Best Local Similarity 82.9%; Pred. No. 1e-28;
Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 131 GGGSDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQKPGKAPKLLIYAASTLQS 190
| | :|||||:| :|||||:| :|||||:| :|||||:| :|||||:| :|||||
Db 18 GARCDIQLTQSPSFLSASIGDRVTITCRASQGIYNYLAWYQKPGKAPKLLIYVASTLQS 77

QY 191 GVPSRFSGSGSGTEFTLTISSLQPEDFGTYCQQLISYPLTFGGGKVEIK 241
|||||:|||||:|||||:|||||:|||||:|||||: :|||||
Db 78 GVPSRFSGSGSGTEFTLTISSLQPEDFASYCQQFNISYPFTFGGKVEIR 128

RESULT 14
S31107
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>

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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:34:05 ; Search time 410.32 Seconds

(without alignments)
206.735 Million cell updates/sec

Title: US-08-779-457-50

Perfect score: 1278
Sequence: 1 QVRLQOSGGGLVQPGKSLRL.....COOLISYPLTFGGGKVEIK 241

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1278	100.0	241	11	US-08-779-457-50
2	1086.5	85.0	251	1	PCT-US01-19110-1310
3	1086.5	85.0	251	22	US-09-880-748-1310
4	1070.5	83.8	251	1	PCT-US01-19110-922
5	1070.5	83.8	251	22	US-09-880-748-922
6	1065.5	83.4	251	1	PCT-US01-19110-1320
7	1065.5	83.4	251	22	US-09-880-748-1320

8	1042.5	81.6	253	1	PCT-US01-19110-936	Sequence 936, App
9	1042.5	81.6	253	22	US-09-880-748-936	Sequence 936, App
10	1040	81.4	242	16	US-09-250-056-2	Sequence 2, Appli
11	1040	81.4	242	16	US-09-250-056B-2	Sequence 2, Appli
12	1040	81.4	244	1	PCT-US01-19110-82	Sequence 82, Appl
13	1040	81.4	244	22	US-09-880-748-82	Sequence 82, Appl
14	1037	81.1	244	1	PCT-US01-19110-261	Sequence 261, App
15	1037	81.1	244	22	US-09-880-748-261	Sequence 261, App
16	1036	81.1	244	1	PCT-US01-19110-164	Sequence 164, App
17	1036	81.1	244	22	US-09-880-748-164	Sequence 164, App
18	1035	81.0	244	1	PCT-US01-19110-280	Sequence 280, App
19	1035	81.0	244	22	US-09-880-748-280	Sequence 280, App
20	1023.5	80.1	239	14	US-09-000-802-15	Sequence 15, Appl
21	1023.5	80.1	248	7	US-08-309-530-6	Sequence 6, Appli
22	1018.5	79.7	243	1	PCT-US01-19110-1945	Sequence 1945, App
23	1018.5	79.7	243	22	US-09-880-748-1945	Sequence 1945, App
24	1011.5	79.1	247	1	PCT-US01-19110-1177	Sequence 1177, App
25	1011.5	79.1	247	22	US-09-880-748-1177	Sequence 1177, App
26	1008.5	78.9	243	1	PCT-US01-19110-1935	Sequence 1935, App
27	1008.5	78.9	243	22	US-09-880-748-1935	Sequence 1935, App
28	1006.5	78.8	237	1	PCT-US01-19110-2043	Sequence 2043, App
29	1006.5	78.8	237	22	US-09-880-748-2043	Sequence 2043, App
30	1004.5	78.6	237	1	PCT-US01-19110-2019	Sequence 2019, App
31	1004.5	78.6	237	22	US-09-880-748-2019	Sequence 2019, App
32	1004.5	78.6	241	1	PCT-US01-19110-1889	Sequence 1889, App
33	1004.5	78.6	241	22	US-09-880-748-1889	Sequence 1889, App
34	1003.5	78.5	237	1	PCT-US01-19110-2003	Sequence 2003, App
35	1003.5	78.5	237	22	US-09-880-748-2003	Sequence 2003, App
36	1003	78.5	248	1	PCT-US01-19110-1421	Sequence 1421, App
37	1003	78.5	248	22	US-09-880-748-1421	Sequence 1421, App
38	1002.5	78.4	237	1	PCT-US01-19110-2005	Sequence 2005, App
39	1002.5	78.4	237	22	US-09-880-748-2005	Sequence 2005, App
40	1002.5	78.4	239	1	PCT-US01-19110-1922	Sequence 1922, App
41	1002.5	78.4	239	22	US-09-880-748-1922	Sequence 1922, App
42	1001.5	78.4	241	1	PCT-US01-19110-1901	Sequence 1901, App
43	1001.5	78.4	241	22	US-09-880-748-1901	Sequence 1901, App
44	1000.5	78.3	237	1	PCT-US01-19110-2040	Sequence 2040, App
45	1000.5	78.3	237	1	PCT-US01-19110-2114	Sequence 2114, App

ALIGNMENTS

RESULT 1
US-08-779-457-50
Sequence 50, Application US/08779457

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: MSX RECEPTOR AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-779-457-50

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Query Match	100.0%;	Score 1278;	DB 11;	Length 241;
Best Local Similarity	100.0%;	Pred. No. 4.9e-102;		
Matches 241;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	QVRLOQSGGGGLVQPRSLRLSLCAASGFTFDDYAMHWVROAPGKGLEWVSGMTWNSGSIGY	60
Db	1	QVRLOQSGGGGLVQPRSLRLSLCAASGFTFDDYAMHWVROAPGKGLEWVSGMTWNSGSIGY	60
QY	61	ADSVKGRFTISRDNAKNSLYLOMSLRAEDTAVYYCAREPHNTDAFDIWRGTLVTWSSG	120
Db	61	ADSVKGRFTISRDNAKNSLYLOMSLRAEDTAVYYCAREPHNTDAFDIWRGTLVTWSSG	120
QY	121	GGGPRGGGGSGGSDVVMQTQSPSLSAFVGDTITTCRASQGIYNYLAWYQQKPKAPKL	180
Db	121	GGGPRGGGGSGGSDVVMQTQSPSLSAFVGDTITTCRASQGIYNYLAWYQQKPKAPKL	180
QY	181	LIYAASTLQSGVPSRFSGSGSGTEFTLTLISSLQPEDEGTYCCQQLISYPLTFGGCTKVEI	240
Db	181	LIYAASTLQSGVPSRFSGSGSGTEFTLTLISSLQPEDEGTYCCQQLISYPLTFGGCTKVEI	240
QY	241	K 241	
Db	241	K 241	

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RESULT      2
PCT-US01-19110-1310
; Sequence 1310, Application PC/TUS0119110

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; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1310

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; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1310

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Query Match	85.0%; Score 1086.5; DB 1; Length 251;
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Best Local Similarity 84.0%; Pred. No. 1.8e-85;
Matches 210; Conservative 10; Mismatches 21; Indels 9; Gaps 1;

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QY      1 QVRLQSSGGGIVOPGRSLRLSCAASGTFEDDYAMHWVRQAAPGKLEWVSGMTNSGSIGY 60
        ||::|||||: | ||||| || ||||| ||||| : : |
Db      1 QVTLKESGGGLYAKAGSLRLSCAASGTFESSYAMTWVRQAAPGKLEWWSAISSGDSASY 60

QY      61 ADSVKGREFTISRDNANKNSLYLQMNSLRADETA VYYCAREPHNTD-----AFDIWGR 111
        ||||| ||||| ::|||:||||| ||||| ||||| : |||
Db      61 ADSVKGREFTISRDNANSKNLTLYLMNSLRADETA VYYCARDPGYYDILTGXFHRYGMVDWGR 120

QY      112 GTLVTVSSGGGPGGGGGSGGGGSDVVMQTSPSFLSAFVGDTTITTCRASOGIYNLYANTQ 171
        || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      121 GTVTVTVSSGGGGSGGGGSDVVMTQSPSFLSAFVGDTTITTCRASOGTYNYLANIQ 180

QY      172 QKP GKAPKL LLYAASTLQS GVPSPRS SSGSGTEFTLTISLSLOPEDFGTY YCCQLISPLT 231
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 QKPGKAPKL LLYAASTLQS GVPSPRS SSGSGTEFTLTISLSLOPEDFGTY YCCQLISPLT 240
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Oy	232	FGG	TKEIK	241
Db	241	FGG	TKEIK	250

```

RESULT      3
US-09-880-748-1310
; Sequence 1310, Application US/09880748
; GENERAL INFORMATION:
;   APPLICANT: Ruben et al.
;   TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;   FILE REFERENCE: PF523
;   CURRENT APPLICATION NUMBER: US/09/880,748
;   PRIOR FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/212,210
;   PRIOR FILING DATE: 2000-06-15
;   PRIOR APPLICATION NUMBER: 60/240,816
;   PRIOR FILING DATE: 2000-10-17
;   PRIOR APPLICATION NUMBER: 60/276,248
;   PRIOR FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/293,499
;   PRIOR FILING DATE: 2001-05-25
;   NUMBER OF SEQ ID NOS: 3239
;   SOFTWARE: Patentln Ver. 2.0
;   SEQ ID NO 1310
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1310

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Query Match	85.0%;	Score 1086.5;	DB 22;	Length 251;
Best Local Similarity	84.0%;	Pred. No. 1.8e-85;		
Matches 210;	Conservative 10;	Mismatches 21;	Indels 9;	Gaps 1;

```

QY      1 QVRLQOOSGGCIVQPCRSRLRLSCAASGTEFDYAMHWVRQAPGKLEWVSGMTWNSGICG 60
      |||:::|||||: | ||||| ||||| ||| ||||| ||||| |||: : | |
Db      1 QVTLKESGGGLYKAGGSLRLSCAASGTEFSSYAMTWVRQAPGKLEWVSAISSGDSASY 60
QY      61 ADSVKGRFTISRDNAKNSLYLQMSLSRAEDTAVYYCCAREPHNTD-----AFDINGR 111
      ||||| ||| |||:::||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCCARDPQYIDILTGYPHRYGMVNGR 120
QY      112 GTLVTVSSGGGGPGGGGGSGGGGSDVYMTQSPSFLSAFVGDTITITCRASQGIYNYLAWQ 171
      ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 GTTVTVSSGGGGSGGGGGSDVYMTQSPSFLSAFVGDTITITCRASQGTNYNYLAWQ 180
QY      172 QKPKAKPKLLIYAAS TLQSGVPSRFSSGSGSTEFTLTISLQPEDFGTYCCQLISYPLT 231
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 QKPKAKPKLLIYAAS TLQSGVPSRFSSGSGSTEFTLTISLQPEDFGTYCCQLISYPLT 240
QY      232 FGGGTKEVEIK 241

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QY 61 ADSVKGRTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTD-----AFDIWGR 111
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Db 61 AESVKGRTISRDNKNSLSLQMSLRAEDTAVYYCARVSPSDILITGYYLPHAFDVGGR 120
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QY 112 GTLVTVSSGGGGGPGGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAWYQ 171
      |||||||
Db 121 GTTVTVSSGGGGGSGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHMLAWYQ 180
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QY 172 QKPKAKPKLLIYAASLTQSGVPSRFSGSGTEFTLTITSSLPEDFGTYCCQLISYPLT 231
      |||||||
Db 181 QKPKAKPKLLIYKASSLASGAPSRFSGSGTDFLTITSSLPDDFAFYCCOYSNYPIT 240
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QY 232 FGGGTKEIK 241
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Db 241 FGGGTKEIK 250
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RESULT 7
US-09-880-748-1320
; Sequence 1320, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1320
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1320
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Query Match 83.4%; Score 1065.5; DB 22; length 251;
Best Local Similarity 80.0%; Pred. No. 1.2e-83;
Matches 200; Conservative 21; Mismatches 20; Indels 9; Gaps 1;
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QY 1 QVRLQSSGGGLVQPGRLRLSCASGFTFDYAMHWVRQAPGKLEWVSGMTWNSGSI 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGVQPGRLRLSCASGFNFDYGMHWVRQAPGKLEWVSGISWNSGTIGY 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADSVKGRTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTD-----AFDIWGR 111
      |||||||
Db 61 AESVKGRTISRDNKNSLSLQMSLRAEDTAVYYCARVSPSDILITGYYLPHAFDVGGR 120
      |||||||
QY 112 GTLVTVSSGGGGGPGGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAWYQ 171
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GTTVTVSSGGGGGSGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHMLAWYQ 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 172 QKPKAKPKLLIYAASLTQSGVPSRFSGSGTEFTLTITSSLPEDFGTYCCQLISYPLT 231
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 QKPKAKPKLLIYKASSLASGAPSRFSGSGTDFLTITSSLPDDFAFYCCOYSNYPIT 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 232 FGGGTKEIK 241
      |||:|||||
Db 241 FGGGTKEIK 250
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RESULT 8
PCT:US01-19110-936
; Sequence 936, Application PC/TUS0119110
```

```
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 936
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-936
```

```
Query Match 81.6%; Score 1042.5; DB 1; length 253;
Best Local Similarity 81.0%; Pred. No. 1.2e-81;
Matches 204; Conservative 12; Mismatches 25; Indels 11; Gaps 2;
```

```
QY 1 QVRLQSSGGGLVQPGRLRLSCASGFTFDYAMHWVRQAPGKLEWVSGMTWNS--GSI 58
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGLVQPGRLRLSCASGFTFDYAMSWFRQAPGKLEWVFIRSKAYGTT 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 59 GYADSVKGRTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTD-----AFDIW 109
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EYASVKGRTISRDKSKSLAYLQMSLKTEDTAVYYCTRAGGYDILTRDYYGMDVW 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 110 GRGTLTVSSGGGGGPGGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAW 169
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GQGTMTVSSGGGGGSGGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAW 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 170 YQKPKAKPKLLIYAASLTQSGVPSRFSGSGTEFTLTITSSLPEDFGTYCCQLISYP 229
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 YQKPKAKPKLLIYAASLTQSGVPSRFSGSGTEFTLTITSSLPEDFGTYCCQLISYP 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 230 LTFGGGTKEIK 241
      |||:|||||
Db 241 LTFGGGTKEIK 252
```

```
RESULT 9
US-09-880-748-936
; Sequence 936, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 936
; LENGTH: 253
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```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-936

```

Query Match	81.6%;	Score 1042.5;	DB 22;	Length 253;
Best Local Similarity	81.0%;	pred. No. 1.2e-81;		
Matches 204; Conservative	12;	Mismatches 25;	Indels 11;	Gaps 2;

[illegible]

```

RESULT 10
US-09-250-056-2
; Sequence 2, Application US/09250056A
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Poul, Marie A
; TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
; FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Ab
; CURRENT APPLICATION NUMBER: US/09/250,056A
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/082,953
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv C1 amino
; FEATURE:
; OTHER INFORMATION: acid sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (31)..(35)
; OTHER INFORMATION: VH-CDR1
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (50)..(66)
; OTHER INFORMATION: VH-CDR2
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (99)..(108)
; OTHER INFORMATION: VH-CDR3
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (157)..(167)
; OTHER INFORMATION: VL-CDR1
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (184)..(190)
; OTHER INFORMATION: VL-CDR2
; FEATURE:
; NAME/KEY: DOMAIN

```

US-09-250-056-2

Query Match	81.4%;	Score 1040;	DB 16;	Length 242;
Best Local Similarity	83.0%;	Pred. No. 1.9e-81;		
Matches 200; Conservative	15;	Mismatches 26;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 11
US-09-250-056B-2
; Sequence 2, Application US/09250056B
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Poul, Marie A
; TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
; FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Ab
; CURRENT APPLICATION NUMBER: US/09/250,056B
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/082,953
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv C1 amino
; OTHER INFORMATION: acid sequence
; NAME/KEY: DOMAIN
; LOCATION: (31)..(35)
; OTHER INFORMATION: VH-CDR1
; NAME/KEY: DOMAIN
; LOCATION: (50)..(66)
; OTHER INFORMATION: VH-CDR2
; NAME/KEY: DOMAIN
; LOCATION: (99)..(108)
; OTHER INFORMATION: VH-CDR3
; NAME/KEY: DOMAIN
; LOCATION: (157)..(167)
; OTHER INFORMATION: VL-CDR1
; NAME/KEY: DOMAIN
; LOCATION: (184)..(190)
; OTHER INFORMATION: VL-CDR2
; NAME/KEY: DOMAIN
; LOCATION: (223)..(231)
; OTHER INFORMATION: VL-CDR3
US-09-250-056B-2

```

Query Match 81.4%; Score 1040; DB 16; Length 242;

Best Local Similarity 83.0%; Pred. No. 1.9e-81;
Matches 200; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

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QY 1 QVRLQSSGGGLVQPGRLRLSCAASGFTFDDYAMHWVROAPGKGLEWVSGMTWNSGSIGY 60
    ||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVESGGGLVQPGSLRLSCAASGFTFSSYAMGVROAPGKGLEWVSSISGSRITYY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMSLRRAEDTAVYYCAREPHNTDAFDINGRGLTVVSSG 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNSLYLQMSLRRAEDTAVYYCAKMDASGSYFNEWGGGLTVTVSSG 120

QY 121 GGGPGGGGGGGSDVYMTQSPSLAFVGDITITTCRASQGIYNYLAWYQOKPGKAPKL 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GGGSGGGGGGGSETTLTQSPSLAFVGDRIITTCRASPGIRNYLAWYQOKPGKAPKL 180

QY 181 LIYAASLTQSGVPSRFRSGSGSGTEFTLTISLQPEDFGTYCCOQLISYPLTFGGGTKEI 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LIYAASLTQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCCOQYNSYPLSRFGGTKEI 240

QY 241 K 241
Db 241 K 241
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RESULT 12

```
PCT-US01-19110-82
; Sequence 82, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-82
```

Query Match 81.4%; Score 1040; DB 1; Length 244;
Best Local Similarity 81.1%; Pred. No. 1.9e-81;
Matches 197; Conservative 17; Mismatches 27; Indels 2; Gaps 1;

```
QY 1 QVRLQSSGGGLVQPGRLRLSCAASGFTFDDYAMHWVROAPGKGLEWVSGMTWNSGSIGY 60
    ||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGLVQPGSLRLSCAASGFTFDDYAMHWVROAPGKGLDWVSATWNSGHIDY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMSLRRAEDTAVYYCAREPH--NTDAFDINGRGLTVVS 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVEGRFAVSRDNKNSLYLQMSLRRAEDTAVYYCTKASYLSTSSSLDNWGGGLTVVS 120

QY 119 SGGGPGGGGGSDVYMTQSPSLAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 178
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SGGGSGGGGGSDIQMTQSPSLASIGDRIITTCRASQGIYNYLAWYQOKPGKAP 180

QY 179 KLIIYAASLTQSGVPSRFRSGSGSGTEFTLTISLQPEDFGTYCCOQLISYPLTFGGGTKEI 238
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KLIIYAASLTQSGVPSRFRSGSGSGTDFTLTISLQPEDVATYYCCQKYNAPYAFGGGTKEI 240

QY 239 EIK 241
```

Db 241 EIK 243

RESULT 13

```
US-09-880-748-82
; Sequence 82, Application us/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-82
```

Query Match 81.4%; Score 1040; DB 22; Length 244;
Best Local Similarity 81.1%; Pred. No. 1.9e-81;
Matches 197; Conservative 17; Mismatches 27; Indels 2; Gaps 1;

```
QY 1 QVRLQSSGGGLVQPGRLRLSCAASGFTFDDYAMHWVROAPGKGLEWVSGMTWNSGSIGY 60
    ||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGLVQPGSLRLSCAASGFTFDDYAMHWVROAPGKGLDWVSATWNSGHIDY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMSLRRAEDTAVYYCAREPH--NTDAFDINGRGLTVVS 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVEGRFAVSRDNKNSLYLQMSLRRAEDTAVYYCTKASYLSTSSSLDNWGGGLTVVS 120

QY 119 SGGGPGGGGGSDVYMTQSPSLAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 178
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SGGGSGGGGGSDIQMTQSPSLASIGDRIITTCRASQGIYNYLAWYQOKPGKAP 180

QY 179 KLIIYAASLTQSGVPSRFRSGSGSGTEFTLTISLQPEDFGTYCCOQLISYPLTFGGGTKEI 238
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KLIIYAASLTQSGVPSRFRSGSGSGTDFTLTISLQPEDVATYYCCQKYNAPYAFGGGTKEI 240

QY 239 EIK 241
Db 241 EIK 243
```

RESULT 14

```
PCT-US01-19110-261
; Sequence 261, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
```


;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 261
;; LENGTH: 244
;; TYPE: PRT
;; ORGANISM: Homo sapiens
PCT-US01-19110-261

Query Match 81.1%; Score 1037; DB 1; Length 244;
Best Local Similarity 80.7%; Pred. No. 3.4e-81;
Matches 196; Conservative 17; Mismatches 28; Indels 2; Gaps 1;

OY 1 QVRLQSGGGLVQPGRLRLSCAAGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGIGY 60
Db 1 QVQLAESGGGLVQPGRLRLSCAAGFTFDDYAMHWVRQAPGKGLDWVSAITWNSGHIDY 60
OY 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPH--NTDAFDIWGRGLVTVS 118
Db 61 ADSVEGRFRAVRSDNAKNALYLQMNSLRPEDTAVYYCTKASYLSTSSLDNWGGTGLVTVS 120
OY 119 SGGGPGGGGGGGSDVVMQSPSLSAFVGDITITCRASQGIYNYLAWYQOKPGKAP 178
Db 121 SGGGSGGGGGGGGGSDIQMTQSPSSLASISIGDRVITTCRASQGITRNYLAWYQOKPGKAP 180
OY 179 KLLIYAASTLQSGVPSRFSGSGTEFTLTITSSLPEDFGTYTCQQLISYPLTFGGGTKV 238
Db 181 KLLIYAASTLQSGVPSRFSGSGTDFLTITSSLPEDVATYYCQKYNAPYAFGGGTKV 240
OY 239 EIK 241
Db 241 EIK 243

RESULT 15
US-09-880-748-261
; Sequence 261, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 261
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-261

Query Match 81.1%; Score 1037; DB 22; Length 244;
Best Local Similarity 80.7%; Pred. No. 3.4e-81;
Matches 196; Conservative 17; Mismatches 28; Indels 2; Gaps 1;

OY 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPH--NTDAFDIWGRGLVTVS 118
Db 61 ADSVEGRFRAVRSDNAKNALYLQMNSLRPEDTAVYYCTKASYLSTSSLDNWGGTGLVTVS 120
OY 119 SGGGPGGGGGGGSDVVMQSPSLSAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 178
Db 121 SGGGSGGGGGGGGGSDIQMTQSPSSLASISIGDRVITTCRASQGITRNYLAWYQOKPGKAP 180
OY 179 KLLIYAASTLQSGVPSRFSGSGTEFTLTITSSLPEDFGTYTCQQLISYPLTFGGGTKV 238
Db 181 KLLIYAASTLQSGVPSRFSGSGTDFLTITSSLPEDVATYYCQKYNAPYAFGGGTKV 240
OY 239 EIK 241
Db 241 EIK 243

Search completed: August 15, 2002, 16:34:06
Job time: 766 sec

OY 1 QVRLQSGGGLVQPGRLRLSCAAGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGIGY 60
Db 1 QVQLAESGGGLVQPGRLRLSCAAGFTFDDYAMHWVRQAPGKGLDWVSAITWNSGHIDY 60

Db 1197 ymptqfqtcsqtgthkkmekmcdltv 1221

RESULT 8

ID AAW34499 standard; protein; 970 AA.

AC AAW34499;

DT 18-MAR-1998 (first entry)

DE Obesity receptor C protein.

XX Obesity receptor; human; OB receptor; OB receptor/OB protein complex;

KW high blood lipid level; obesity; diabetes; high cholesterol level;

KW weight loss; therapy; weight maintenance.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 959 /label= unknown

FT /note= "encoded by stop codon"

PN W09725424-A1.

PD 17-JUL-1997.

PF 02-JAN-1997; 97WO-US00128.

PR 31-DEC-1996; 96US-0774414.

PR 04-JAN-1996; 96US-0582825.

PA (AMGE-) AMGEN INC.

PI Chang M, Fletcher FA, Welcher AA;

XX WPI: 1997-384981/35.

DR N-PSDB; AAT98530.

XX Obesity protein receptor(s) and related DNA - used to treat weight

PT disorders, e.g. obesity, diabetes and high cholesterol or blood

PT lipid levels

XX Claim 2; Page 72; 151pp; English.

XX This sequence represents the obesity (OB) receptor C protein. This

CC sequence has one or more of the biological properties of naturally

CC occurring OB receptor protein. The OB receptor proteins and OB

CC receptor/OB protein complexes are used for the treatment of obesity,

CC diabetes, high blood lipid levels and high cholesterol levels. The

CC proteins may also be used to treat an individual for weight loss or

CC weight maintenance required for purely cosmetic purposes.

XX Sequence 970 AA;

QY 1 MICQKFCVVLHWEFIVITAFNLSTPTPWRFKLSCMPNSTYDYFLLPAGISKNTSNS 60

Db 1 micqkfcvvlhweftvitaftnlsypitpwrfkiscmpnstydyfllpagiskntsns 60

QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSVNSLVF 120

Db 61 nghyetavepkfnsqthfnslskttfhccfrseqdncslcadniegkttfsvnslvf 120

QY 121 QCIDANMNIIQCWLKGLDLFLICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 180

Db 121 qcidanwniqcwlkglklficyveslfknlfirnykvhllylvplevledsplvpqkgs 180

QY 181 FQMVHNCNVHECCCLVPVPTAKLNDTLMLCKLITSGVIFQSPILMSVQPINMVKPDPP 240

Db 181 fgmvhncnsvhecceclvpyptaklndtlmlcklitsgvi fqsplmsvqpinmvkpdpp 240

QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKSSENSITVIREADKIVSATSLLDVSIIP 300

Db 241 lglhmeitddgnlkiswsspplvfpplqyqvksensitvireadklvsatslldvsiip 300

QY 301 GSSYEVQVRGKRDLDPGILMSDSTPRVFTTQDYVTFPPKILTSVGSNVSFHCITYKKENKI 360

Db 301 gssyevqvrgrldpgilmsdstprvfttdyvtfpkiltsvgsnvsfnciykknki 360

QY 361 VPSKEIVMMNLAEKIPQSOYDVSDHVSKVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420

Db 361 vpskeivmmnlækipqsqydvsvdhvskvtfpflnetkprgkftdyavycnehechh 420

QY 421 RYAEIYVIDVNNINISCEITDGYLTMTCRWSTSTIQLAESTLQLRYHRSLSYCSDIPIIH 480

Db 421 ryaelvyidvnniniscedtgyltmtcrwststqlaestlqlryhrsslycsdipih 480

QY 481 PISEPKDCYILOSDFEYECIFQPIFLISGYTMTIRINSLGSLDSPPTCVLPDSVVKPLPP 540

Db 481 pisepkdcylqsdgfyecifqipifllsgytmtrlnslsglsdspptcvlpdsavvkplpp 540

QY 541 SSVKAEITINIGLKLISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600

Db 541 ssvkaeitiniglkliswekvpfpennlofquiryglsgkevqwmvevydaksksvslpv 600

QY 601 PDLCAVYAVQVRCKRDLGLGYSNWSNPATYVWDIKVPMRGPEFWRIINGDTMKKEKNV 660

Db 601 pdlcavyavvrckrldglgysnwsnpatyvwdikvpmrgpewrilingdtmkkeknv 660

QY 661 TLWKPLMKNDLSQVQRYVINHTSCNGIWSDEVGNHTKFTFLWTEQAHTVTLAINSI 720

Db 661 tlwkplmkndlsqvqryvinhtscngiwsedvgnhtkftflwteqahvtvlainsi 720

QY 721 GASVANFNLTFSWPMKVNIVQSLASAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 780

Db 721 gasvanfnltfswpmkvnivqslasayplnnsctvswilspdyklyfiemknlne 780

QY 781 GEIKWLRISSSVKXYIHDFTPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840

Db 781 geikwlri:sssvkxyihdftpiekyqfslypifmegvgkpkinsftoddiekhqsd 840

QY 841 GLYIVIPVLISSSILLGTLTLLISHQRMKTLFWEDVPNPKNCSWAAGLNFQK-----PE 893

Db 841 glyvivpvlisslillgtllishqrmkklfwedvpnpkncswaglnfgqlmlegsmfvk 900

QY 894 TFEHLFIKHT-ASYTCGP-----LLEPETISEDISVDTSWKNKDE 933

Db 901 shhslisstqghkncgrpgpplrktldcslvlltllppllsydpakpsvrvntqe 958

RESULT 9

ID AAW24052 standard; Protein; 896 AA.

AC AAW24052;

DT 17-MAR-1998 (first entry)

DE Human WSX receptor variant 6.4.

XX Human; WSX receptor; variant 6.4; identification; purification;

KW ligand; activator; antibody; agonist; proliferation; obesity;

KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;

KW Type II diabetes; polycystic ovarian disease;

KW cardiovascular disease; osteoarthritis; dermatological disorder;

KW hypertension; insulin resistance; hypercholesterolaemia;

XX hypertriglyceridaemia; cancer; cholelithiasis.

OS Homo sapiens.

XX WO9725425-A1.
PN 17-JUL-1997.
PD 07-JAN-1997; 97WO-US00325.
PE 20-JUN-1996; 96US-0667197.
PR 08-JAN-1996; 96US-0585005.
XX (GETH) GENENTECH INC.
XX Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX WPI; 1997-372864/34.
DR N-PSDB; AAT85576.
XX MSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
XX
PS Claim 2; Pages 86-89; 219pp; English.
XX The present sequence is the human MSX receptor variant 6.4,
CC which can be used to identify and purify ligands and activators.
CC An anti-MSX receptor antibody can be used as an agonist to activate
CC the MSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the MSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. MSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
XX
XX Sequence 896 AA;
SQ

Query Match 77.2%; Score 4826; DB 18; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSTPTPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60
DB 1 micqkfcvllhweiyvitafnlstptpwrfklscompnstydyflpaglskntsns 60
QY 61 NGHYETAVEEKFNSGTHFNSLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 nghyetaveepkfnsqthfnslskttfhccfrseqdrncslcadniegkttvstvnslvf 120
QY 121 QOIDANNNIOQWLKGDCLKFICYVESLEFKNLFRNNYKVKHLLVLPVLEDSPLVPQKGS 180
DB 121 qqidanwniqcwlkgdclkficyveslfknlfrrnykvhllylvpevledsplvpqkgs 180
QY 181 FQMVHCNCSYHCECECLVPVPTAKLNDITLMCLKITSQGVIFQSPILMSVQPINMVKPDPP 240
DB 181 fgmvhcnscyhcececlvpvptaklnditlmclkitsgvifqspilmsvqpinmvkpdpp 240
QY 241 LGLHMEITDGNLKLISWSSPPLVPPELOYKYSENSTVIREADKIIVSATSLVDSTLP 300
DB 241 lglhmeitdgnlkliswsspplvpfpdyqvykysenstvireadkiivsatslvdslp 300
QY 301 GSSYEVOYRGKRLDGPISWSDWSTPRVETQDVIYFPKILTSVGSNVSFHCITYKKENKI 360
DB 301 gssyevoyrgkrlldgpgiwsdwtprvftqdvlyfppkiltsvgsnvsfhciykenki 360

QY 361 VPSKEIWMNNLAEKIPQSOYDVVSDHVSQVTFEENLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 vpskeiwmnnlaekipqsqydvvsdhvskvtfeennetkprgkfttydavyccnehechh 420
QY 421 RYAEIYVIDVNNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480
DB 421 ryaeliyvidvnniniscetdgylltkmcrwststlqslaestlqlrhrslycsdipsih 480
QY 481 PISEPKDCYLSQDGFECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 pisepkdcylsqdgfyecifqipifllsgytmirinhslsglsdspptcvlpdsvvkplpp 540
QY 541 SSVKAEITINIGLKISWEKPVPEENNLOFQIRYGLSGKEVQWKMKEVYDAKSQSVSLPV 600
DB 541 ssvkaeitiniglkiswekpvpeennlqfityrglsqkevqwmkevydaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSMNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKREKNV 660
DB 601 pdlcavyavqvrckrlldglgywsnwnspaytvvmdikvpmrgpefwrilingdtmkreknv 660
QY 661 TLLMKPLMKNDISGVQRYVINHTSCNGTWSSEYGNHTKFTFLWTEQAHVTYVLAINSI 720
DB 661 tllwkpmlkndislesvqryvinhtscngtwsedvgnhtkftflwteqahvtvlainsi 720
QY 721 GASVANFNLTFSWPMKVNIVQSLASAYPLNSGCVISWILSPSDYKLMFIEMKNLNE 780
DB 721 gasvanfnltfswpmkvnivqslasayplnsscvlswilspdyklmfielwnlne 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLPMEGVGKPKIINSFTODDIEKHOSDA 840
DB 781 geikwlriSSsvkyyihdhfipiekYqfslpimegvGkpkiinsftoddiekhgsda 840
QY 841 GLYIVPVITISSSILLGLTLISHQRMKKLFWEDVPNPKNSWAQGLNFGK 891
DB 841 glyivpvitissSillgltlilshqrmkklfweDvpnpknCswaQglNfgk 891

RESULT 10
AAW24053
ID AAW24053 standard; Protein; 923 AA.
XX
AC AAW24053;
XX
DT 17-MAR-1998 (first entry)
XX
DE Human MSX receptor variant 12.1.
XX
KW Human; MSX receptor; variant 12.1; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW Type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.
XX
OS Homo sapiens.
XX
PN WO9725425-A1.
XX
PD 17-JUL-1997.
XX
PE 07-JAN-1997; 97WO-US00325.
XX
PR 20-JUN-1996; 96US-0667197.
PR 08-JAN-1996; 96US-0585005.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX WPI; 1997-372864/34.

DR N-PSDB; AAT85577.
XX
PT WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
XX
PS Claim 2; Pages 89-93; 219pp; English.
XX
CC The present sequence is the human WSX receptor variant 12.1,
CC which can be used to identify and purify ligands and activators.
CC An anti-WSX receptor antibody can be used as an agonist to activate
CC the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. WSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
XX
XX
SO Sequence 923 AA;

Query Match 77.2%; Score 4826; DB 18; Length 923;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFTVITAFNLSPITPMRFKLSGMPNSTYDYFLLPAGLSKNTNS 60
Db 1 micqkfcvllhweftvitatfnlsypitpwrflkscmpnstydyfllpaglsknts 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVSLVF 120
Db 61 nghyetavepkfnssgthfnslsttfhccfrseqdrcnslcadniegkctfvstvnslvf 120
QY 121 QOIDANMNIQCWLKGLKLEFCYVESLFEKNLFRNRYKVHLLVLPVLEDSPLVPQGS 180
Db 121 qoidanwniqcwlkgdlkelfcyveslfnknlfrynkvhllvlpvledsplaypqgs 180
QY 181 FOMVHCNCSVHECCCLVPPYPAKLNDTLMCLKITSGVIFQSPMSVQPINMVKPDP 240
Db 181 fgmvhcnscvheccclvpyptaklndtlmclkitsgvifqspmsvqpinmvkpdpp 240
QY 241 IGLHMEITDDGNLKISWSPPLPVPELOYOVKYSNSTTVIREADKIVSATSLVDSILP 300
Db 241 lglhmeitddgnlkiswspplpvpfloyovkysensttvireadkivsatslvdsilp 300
QY 301 GSSYEYQVRGKRLDGPGLMSDMPSTPRVFTQDVITFPFKILTSVGSNVSFHCITYKKENKI 360
Db 301 gssyevqvrgrldgpglmsdstprvftqdvityfpfkiltsvgsnvsfhciykkenki 360
QY 361 VPSKEIVMMMLAEKIPQSDYDVSDHVKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 vpskeivwmmlaekipqsgdydvsdhsvkvtfflnetkprgkftlydavycnehechh 420
QY 421 RYAEIVVIDNININISCEPDGYLTMTCRWSTSTIQSLAESTLQLRYHRSLSYCSDIPTSH 480
Db 421 ryaelyvividnininiscedgyltmcrwststiqslaestlqlryhrsslycsdipsh 480
QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTMMIRINHSLGSLDSPPTCYLPDSVYKPLP 540
Db 481 ptsepkdcylqsdgfyecifqipifllsgytmmirinhslgsldspptcylvsvykpplp 540
QY 541 SSVKAETITINIGLKISWEKVPENNLQFQIRYGLSGKEVQWKMYEVDYDAKSKSVSLPV 600
Db 541 ssvkaeitiniglkiswekvpennlqfqi ryglsqkevqwkmyevdydaksksvslpv 600

QY 601 PDLCAVYAVQVRCRLDGLGYSNWSNPATVVMMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 pdlcavayavqrckrldglgysnwsnpaytvvmmdikvpmrgpefwrlingdtmkkeknv 660
QY 661 TLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSDEVGNHTKFTFLMTQEAHTVTLAINSI 720
Db 661 tlwkplmkndslcsvqryvinhhtscngtwsedvgnhtkftflwteqahvtvlainsi 720
QY 721 GASVANFNLTFSWPMKVNIVQSLSAYPLNSSCVIVSNILSPSDKLMYFIIEWKNLNED 780
Db 721 gasvanfnltfswpmskvnivqslsayplnsscviwslpsdyklimyfiiewknled 780
QY 781 GEIKWLRISSSVKKYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 gelkwlrissvkkynidhpipekyqfslypifmegvgkpkilnsftqddiekhsda 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFEWEDVPNPKNCWAQGLNFOK 891
Db 841 glyvivpviissillgltllishqrmkklfwedvpnpkncswaqglnfqk 891

RESULT 11

AAW34497 ID AAW34497 standard; protein; 972 AA.

XX AC AAW34497;

XX DT 18-MAR-1998 (first entry)

XX DE Obesity receptor A protein.

XX KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;

KW high blood lipid level; obesity; diabetes; high cholesterol level;

KW weight loss; therapy; weight maintenance.

XX OS Homo sapiens.

XX FH key Location/Qualifiers

FT Misc-difference 897 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 919 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 925 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 939 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 948 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 952 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 971 /label= unknown

FT /note= "encoded by stop codon"

XX PN W09725424-A1.

XX PD 17-JUL-1997.

XX PF 02-JAN-1997; 97WO-US00128.

XX PR 31-DEC-1996; 96US-0774414.

XX PR 04-JAN-1996; 96US-0582825.

XX PA (AMGE-) AMGEN INC.

XX PI Chang M, Fletcher FA, Welcher AA;

XX WPI: 1997-384981/35.
DR N-PSDB; AAT98528.
XX
PT Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX
PS Claim 1; Page 64; 151pp; English.
XX
CC This sequence represents the obesity (OB) receptor A protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX
SQ Sequence 972 AA;

Query Match 77.2%; Score 4826; DB 18; Length 972;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MICCKFCVLLHMEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTNS 60
DB 1 mtcqkfcvllhweifyltafnlstypitpwrfklscmpnstydyfllpaglskntns 60
OY 61 NGHYETAVEPKFNSSGTHFSNLSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSTLV 120
DB 61 nghyetavepkfnssgthfnslsttfhccfrseqdrcnslcadniegkftfvstvnslvf 120
OY 121 QQIDANMNIQCWLKDKLFTCYVESLFKNLFRNYKYVHLVLPVLEDSPLVPQKS 180
DB 121 qqidanmniqcwldklftcyveslfnlfrnykyvhlvlpvledsplvpqks 180
OY 181 FQMYHCNCSVHECCCLVPPVPAKLNDTLMLCLKITSQGVIFQSPMSVQPIIMVKPDP 240
DB 181 fqmwhcnscsvheccclvppvpaklndtlmlclkitsgvlfqsplmsvqplimvkdpp 240
OY 241 LGHMEITDDGNLKISWSSPPIVPEPLQYQVKSSENSTVIRADKIVSATSLVDSILP 300
DB 241 lghmeitddgnlkiswssppivpeplqyqvkssensstviradkivsatslvdslp 300
OY 301 GSSYEYQVRGKRLDGPGLWSDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKEN 360
DB 301 gssyeyvrgkrlldgpglwsdstprvfttqdvlyfppkiltsvgsnvsfhcitykknk 360
OY 361 VPSKEIWMWMLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
DB 361 vpskeiwmwmlaekipqsgydvvsdhvskvtfenlnetkprgkfttydavycnehech 420
OY 421 RYAEIYVIDVININISCEITDGYLTMTCRWSTSTIOSLAESTIQLRYHRSSLYCSDIPS 480
DB 421 ryaelyvdivniniscetdgyltmtcrwststioslaestlqlryhrsslycsdipsih 480
OY 481 PISEPKDCYLQSDGFYECIFDPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLP 540
DB 481 pisepkdcylqsdgfyecifdpifllsgytmwirinhslsdpsptcplpdsvvkplp 540
OY 541 SSYKAEITINIGLKLISWEKPYEPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLP 600
DB 541 ssykaeitinigllkliswekpyepennlofquiryglsgkevqwkmyevydaaksksvslp 600
OY 601 PDICAVYAVQVRCKRLDGLGYSWMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKN 660
DB 601 pdicavyavvrckrldglgyswmsnpaytvvmdikvpmrgpewrriingdtmkkekkn 660
OY 661 TLWKPLMKNDLSGVQRYVINHTSCNGTMSSEDEVGNHTKFTFLWTEQAHVTVLAINSI 720
DB 661 tlwkpmlkndlsqvgryvinhtscngtmssedevgnhtkftflwteqahvtvlainsi 720

OY 721 GASVANFNLTFSWPMKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
DB 721 gasvanfnltfswpmkvnivqslsavplnsscvivswilspdyklymfiemknlne 780
OY 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840
DB 781 geikwlri:sssvkkyihdhfpi:ekyqfslypi:fmegv:gpki:insftoddiekhgsda 840
OY 841 GLYVIVPVIISSTILLGTLTISHQRMKLFWEDEVNPNKNCWAQGLNFQK 891
DB 841 glyvivpviisssillgtllshqrmklfwedvnpnkncswaqglnfqk 891

RESULT 12
ID AAW34498 standard; protein; 999 AA.
XX
AC AAW34498;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor B protein.
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 905 /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 933 /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 971 /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 988 /label= unknown
FT /note= "encoded by stop codon"
FT /label= unknown
FT /note= "encoded by stop codon"
PN WO9725424-A1.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US00128.
XX
PR 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M, Fletcher FA, Welcher AA;
XX
DR WPI: 1997-384981/35.
DR N-PSDB; AAT98529.
XX
PT Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX
PS Claim 2; Page 68; 151pp; English.
XX
CC This sequence represents the obesity (OB) receptor B protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX

Sequence 999 AA;

Query Match 77.2%; Score 4826; DB 18; Length 999;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIVITAFNLSYPTIPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
DB 1 micqkfcvllhweifyltafnlsyptipwrfklscompnstydyfllpaglskntsns 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 nghyetavepkfnssgthfnslnsktfhccfrseqdncslcadniegktfvstvnslvf 120
QY 121 QOIDANMNIQCWLKGDILFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
DB 121 qoidanwniqcwlkgdilkficyveslfknlfrnykvhllylvplevedsplvpqkgs 180
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVTFQSPILMSVQPINMVKPDPP 240
DB 181 fgmvhcnscvheccceclvpyptaklndtlmlclkitsgvtfqsplmsvqpinmvpkpdpp 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 lglhmeitddgnlkiswsspplvpfploqyqvkysensttvireadkivsatsllvdsilp 300
QY 301 GSSYEYQVRGKRLDGPGLWSDMSTPRVFTTQDVYIFPPKILTSVGSNVSFHCIYKKNKI 360
DB 301 gssyevqvrgrldgpglwsdswstprvfttqdvlyfppkiltsvgsnvshciykknki 360
QY 361 VPSKEIWMNNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAYVCCNEHECHH 420
DB 361 vpskeiwmnnlaekipqsqydvsvdhvskvtfeflnetkprgkftydavycchh 420
QY 421 RYAEIYVIDVNNINISCTDGYLTMTCRWSTSTQSLAESTLQRLRYHRSLSYCSIPSTH 480
DB 421 ryaelyvldvnniniscetdgyltmtcrwststqslaestlqrlryhrsslycsdpsih 480
QY 481 PISEPKDCYLQSDGFECTFQPIFLSGVTWIRNHSIGSLDSPTCVLPDVSVPKPLP 540
DB 481 pisepkdcylqsdgfyecfipflisgytwtwlrnhsigslsdpsptcvlpdsvvpkplp 540
QY 541 SSVKAEITINIGLKIEMKRVFEPENNLQFOIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
DB 541 ssvkaeitiniglkisemkrvfepennlqfoiryglsqkevqwmvevydaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSNMSNPATYVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660
DB 601 pdlcavayavqvrckrldglgysnmsnpatytvmdikvpmrgpewrriingdtmkkeknv 660
QY 661 TLLMKPLMKNDLSLCSVORVYVNNHTSCNGTWSSEVDCNHTKFTPLMTEQAHVTVLAINSI 720
DB 661 tllmkplmkndslcsvorvynnhhtscngtwsedvgnhtkftplmteqahvtvlainsi 720
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNNSCVIVSWILSPSDYKLMYFTIEMKNLNEED 780
DB 721 gasvanfnltfswpmksvniqslsayplnnsctvswilspdyklmyftiemknlneed 780
QY 781 GEIKWLRISSSVKKYVYHDFPIPIEKYQFSLYPIFMEGVGKPKTIINSFTQDDIEKHQSDA 840
DB 781 gelkwlri:sssvkkyvindhfpiekyqfslypifmegvgkpktiinsftqddiekhsda 840
QY 841 GLYVIVPVISSSILGLTLLISHQRMKILFWEDVPNPKNCSWAQGLNFQK 891
DB 841 glyvivpvi:sssillgtllishqrmkilfwedvpnpknscswagqlnfqk 891

RESULT 13
ID AAW38214 standard; Protein; 958 AA.
XX
AC AAW38214;

XX 11-JUN-1998 (first entry)
DT Human OB-R variant Form 1.
XX
XX *
KW Detection; defective obese protein receptor; defective OB-R; human;
KM defective leptin receptor; variant Form 1; infertility.
XX
OS Homo sapiens.
XX
PN WO9741263-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-US07676.
XX
PR 29-APR-1996; 96US-0640389.
XX
PA (PROG-) PROGENITOR INC.
XX
PI Clotfi J, Shafer AW, Snodgrass RH, Zupancic TJ;
XX
DR WPI; 1997-549757/50.
DR N-PSDB; AAT95779.
XX
PT Detecting defective obese protein or leptin receptor in reproductive
cells - using variant receptor gene specific probes
XX
PS Disclosure; Fig 3; 40pp; English.

CC The present sequence was used in the development of a novel method
CC for detecting a defective obese protein or leptin receptor (OB-R)
CC in cells. Them method comprises contacting RNA extracted from a
CC cell population (preferably an ovary, prostate, testis, sperm, ova,
CC ovarian follicular or blood cell population) with an
CC oligonucleotide derived from a portion of the human OB-R variant
CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
CC associated with infertility, as they are unable to correctly
CC transduce signals from leptin binding. The detection method can be
CC used to diagnose infertility, or predisposition to infertility,
CC while treatments that inhibit or down regulate the variants, gene
CC therapy to replace them in homozygotes or direct activation of
CC downstream signal transduction can be used to improve fertility.
CC Also described is the use of labelled DNA probes based on the OB-R
CC sequence to screen for other variants.
XX
SQ Sequence 958 AA;

Query Match 77.1%; Score 4819.5; DB 18; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHMEFIVITAFNLSYPTIPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
DB 1 micqkfcvllhweifyltafnlsyptipwrfklscompnstydyfllpaglskntsns 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 nghyetavepkfnssgthfnslnsktfhccfrseqdncslcadniegktfvstvnslvf 120
QY 121 QOIDANMNIQCWLKGDILFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
DB 121 qoidanwniqcwlkgdilkficyveslfknlfrnykvhllylvplevedsplvpqkgs 180
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVTFQSPILMSVQPINMVKPDPP 240
DB 181 fgmvhcnscvheccceclvpyptaklndtlmlclkitsgvtfqsplmsvqpinmvpkpdpp 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 lglhmeitddgnlkiswsspplvpfploqyqvkysensttvireadkivsatsllvdsilp 300

QY 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVLYEPKILTSVGSNVSHCIYKKENKI 360
Db 301 gssyeqvgrkrlidgplwsdstprvfttqdvlyfppkiltsvgsnvshfchlykckenki 360
QY 361 VPSKEIIVMMNLAEKIPQSQYDVSDHVSQVTFEENLNETKPRGKFTYDAYVCCNEHECHH 420
Db 361 vpskeivmmnlakelpsqdydvshvskvtfefnlnektprgkfttydayvccnehechh 420
QY 421 RYAEIYVIDVININISCESTDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 ryaeliyvidvininiscetdgyltkmtcrwststlqslaelstqlryhrsslycsdipsih 480
QY 481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
Db 481 pisepkdcylsgdfyecifqpifllsgytmwirinhsllsgldspptcvtlpdsvvkplrp 540
QY 541 SSVKAEITINIGLKISWEKVPFPEENLQFQIRYGLSGKEVQWKMVEYVDKSKSVSLPV 600
Db 541 ssvkaeltinlglikiswekvpfpenlqfqrlyglsqkevqwmvevydaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKREKNV 660
Db 601 pdlcavyavvrckrlidglgywsnwnspatvymdikvpmrgpefwrilingdtmkckeknv 660
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTSEEDVGNHTKFTPLWTEQAHVTVLAINSI 720
Db 661 tllmkplmkndslcsvqryvinhhtscngtseedvgnhtkftplwteqahvtvlainsi 720
QY 721 GASVANFNLTFSWPMKVNIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNEED 780
Db 721 gasvanfnltfswpmkvnivovslsayplnnsccvsvswilspdyklymfielwknlned 780
QY 781 GEIKWLRISSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFWODDIEKHQSDA 840
Db 781 geikwlri:sssvkkyihdhfipiekqfslypifmegvgkpkilnsftgddiekhsda 840
QY 841 GLYVIVPVISSSILGLTLLISHQRMKLFWEDEVNPNKCSWAQGLNFQK-----PE 893
Db 841 glyvivpvi:sssillgtllishqrmklfwedevpnkncswaqglnfqkmlqsgsmfvk 900
QY 894 TFEHLFIKHT-ASVWCGP-----LLEPETISEDISVDTSNKNKDE 933
Db 901 shhslisstqghkhogrpqgplhrktrdclslvyltltpllslsydpakspsvntqge 958

RESULT 14
ID AAW31911 standard; Protein; 958 AA.
XX AAW31911;
AC AAW31911;
XX 02-FEB-1998 (first entry)
DT
XX
DE Human OB-R leptin receptor variant.
XX
KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
KM diagnosis; human.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Misc-difference 85 /note- "variation from published sequence"
FT Misc-difference 109 /note- "variation from published sequence"
FT Misc-difference 223 /note- "variation from published sequence"
FT Misc-difference 845..862 /note- "variation from published sequence"
FT Domain /label- Transmembrane_domain
FT Misc-difference 892..958 /note- "divergence from published sequence"
FT
XX
PN WC09726370-A1.

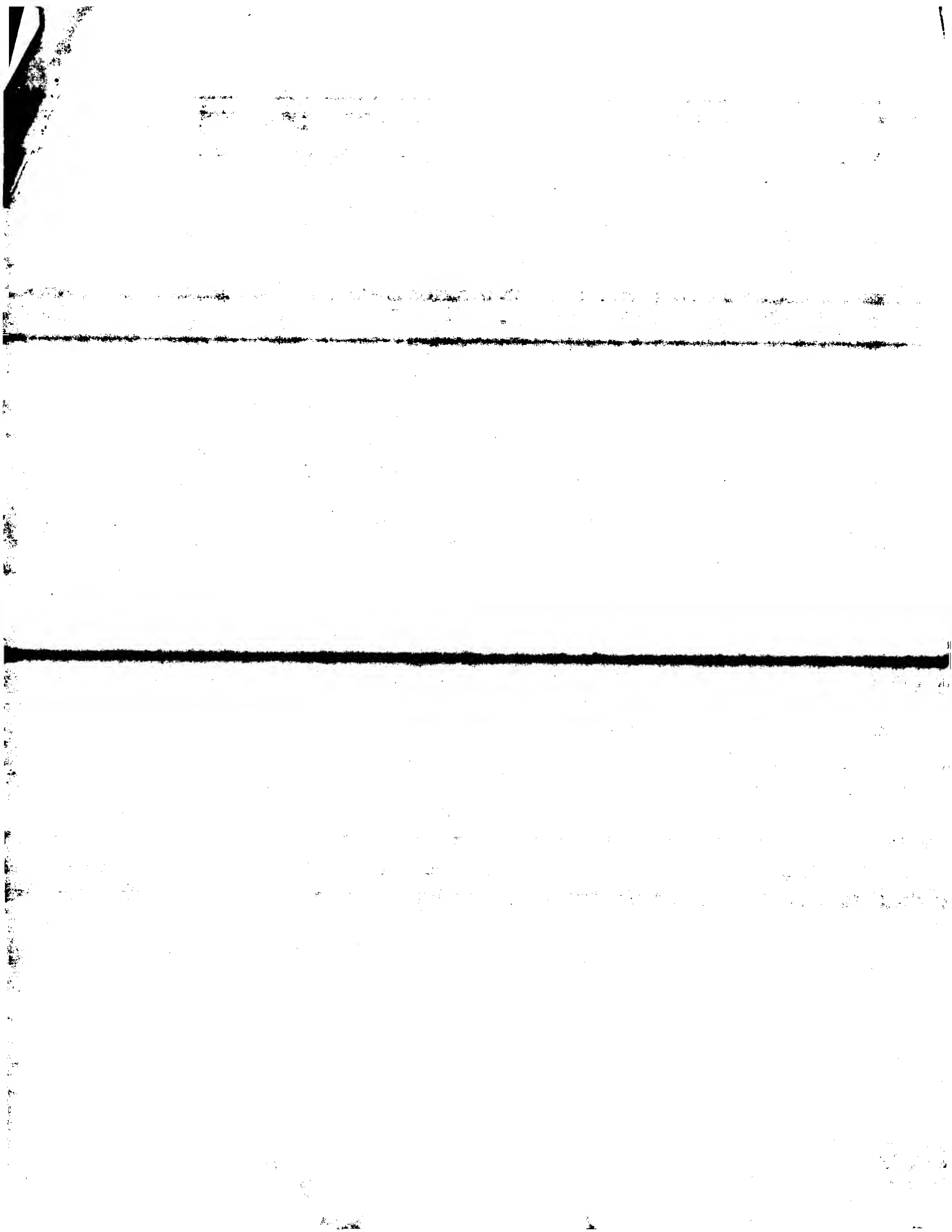
XX 24-JUL-1997.
PD
XX
PF 17-JAN-1997; - 97WO-US00570.
XX
PR 18-JAN-1996; 96US-0588190.
XX
PA (PROG-) PROGENITOR INC.
XX
PI Clotfi J, Shafer AM, Snodgrass HR, Zupancic TJ;
XX
DR WPI: 1997-385353/35.
DR N-PSDB; AAT89193.
XX
XX
PT Detecting defective leptin receptor by hybridisation assay - and
PT treatment of obesity with agent that inhibits the defective
PT receptor, also screening for compounds that supplement leptin
PT activity
XX
PS Claim 12; Fig 1A-E; 26pp; English.
XX
CC This polypeptide comprises a variant of the human leptin receptor
CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193)
CC derived from overlapping clones isolated from a human foetal liver
CC library. The sequence shows near identity to a published OB-R
CC sequence in the extracellular domain, with the exception of 3 amino
CC acids, but there is extensive diversity in the intracellular
CC cytoplasmic domain at the C-terminal end. A claimed method for
CC detection of OB-R in cells comprises extraction of RNA and testing
CC this for hybridisation to an oligonucleotide (1) derived from the
CC OB-R variant gene, especially from the region beyond nucleotide
CC 2770. Also claimed are methods of: (1) treating obesity by
CC administration of an agent that inhibits expression of the OB-R
CC variant gene; and (2) identification of a compound that can
CC supplement activity of leptin by: (1) incubating cells expressing
CC OB-R variant first with leptin and then with a test compound, and
CC (11) comparing activation signals between cells treated and not
CC treated with the test compound. Inhibition/down-regulation of the
CC variant OB-R (found in obese people) improves response of cells to
CC weight regulation by leptin. Replacing variant OB-R by gene therapy
CC (in homozygous individuals) can be used to treat obesity. Labelled
CC probes based on the gene can be used to isolate other variant forms
CC of the receptor gene or to detect the variant gene (e.g. for
CC determining predisposition to obesity), while the OB-R gene can be
CC used to express recombinant OB-R (optionally as fusion protein) and
CC in standard hybridisation assays. The OB-R gene can also be used
CC therapeutically in cases of overexpression of functional OB-R
CC (causing loss of appetite and hypermetabolic activity). Cells
CC engineered to express variant receptor are used in method (2) to
CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
CC antibodies that competitively inhibit, neutralise or enhance activity
CC of the variant receptor.
XX
SQ Sequence 958 AA;

Query Match 77.1%; Score 4819.5; DB 18; Length 958;
Best local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHWEFTVITAENLSYPTPWRFKLSCMPNPNSTYDYFLPAGLSKNTSNS 60
Db 1 micqkfcvllhweftvitaenlsyptpwrfklscompnstydyflpagskntsns 60
QY 61 NGHYETAVEPKFNSGTHHSNLSKTYTHCCFRSEQDRNCSLCADNIEGKTFVTVNSLVF 120
Db 61 nghyetavepkfnsghhsnlsktythccfrseqdrncslcadniegktfvtnslvf 120
QY 121 QOIDAMNIOCWLGDKLFCYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 180
Db 121 qoidamniocwlgdklfcyveslfknlfrnykvvhllvlpvledsplvpqkgs 180
QY 181 FQMVHCNCSVHECCELVVPYTAKLNDTLMLCKLITSGCVIFQSPLMSTVQPINWYKPPDP 240


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|||||
Db 61 nghyetavepkfnssgthfnlskathccfrseqdnscslcadniegrlfvstvnslvf 120
QY 121 QOIDANMNIQCWLKGLKLFICYVESLFKNLFRNYNKVHLVLPVELEDSPLVPQGS 180
Db 121 qqldanwnlqgwklgdklficyveslfnlfrnykvhllylpeveledsplvpqks 180
QY 181 FQWVHCNCSVHECCCEIVPVPTAKLNDTLMLCLKITSGVIFQSPLMVSQPINWKPDP 240
Db 181 fgmvhncsvheccceciivpyptaklndtlmclkitsgvifrsplmsvqpinmwkpdpp 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPEPLQYQVKSSENSTVIREADKIVSATSLYDSILP 300
Db 241 lglhmeitddgnlkiswsspplvpplqyqvkysenstlvireadkivsatsllydsilp 300
QY 301 GSSYEYQVRGKRLDGPFGIWSMDSTPRVFTTQDVYIFPPKILTSVGSNVSEHCYKKNKI 360
Db 301 gssyeqvgrkrlldgpglwsdstprvfttqdvlyfppklltsvgsnvshciykenki 360
QY 361 VPSKEIWWMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 vpskeiwwmmnlaeqipqsqydvsdhvsqvtfeflnetkprgkftydavycnehechh 420
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Db 421 ryaelyvidvninisceitdgyltmtcrwststislaestlqlrhrsslycsdipsih 480
QY 481 PISEPKDCYLQSDGFYECIFQIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 pisepkdcylqsdgyfeciifqifllsgytmwirinhsigslsdpptcvlpdsvvkplpp 540
QY 541 SSVKAEITINIGLTKISWEKVPPENNLOQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db 541 ssvkaeitinigltkiswekvppeennloqirylsgkevqwkmyevydaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 pdlcavyavvrckrldglgywsnmnsnpatylvmdikvpmrgpewrilingdtmkkeknv 660
QY 661 TLLMKPLMKNDLSQVQRYVINNHTSCNGTWESEVGNHTKFTFLWTEQAHVTYLAINSI 720
Db 661 tllmkplmkndlsqvqryvinhntscngtwsedvgnhtkftflwteqahvtvlayainsi 720
QY 721 GASVANENLTFSEWMSKVINQSLAYPLNNSCYIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 721 gasvanenltfsewmskvinqslasayplnnsctyivswilspdyklimyfiiewknlne 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDITEKHQSDA 840
Db 781 geikwlri:sssvkyyihdhfipiekysfslpifmegvgkpkliinsftqddiekhsda 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKLFWEDEVNPNKNCSWAOGLENFQK-----PE 893
Db 841 glyvivpviisssillgltllishqrmklfwevnpnkncswaqlnfqkmelegssfvk 900
QY 894 TFEHLFIKHT-ASVTGCP-----LLEPETISEDISVDTSMKNKDE 933
Db 901 shhsli:stqgkhcgprpgplhrktrd:slvylitl:lppllsydpakspsvrntge 958
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Search completed: August 15, 2002, 16:24:03
Job time: 313 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 16:15:10 ; Search time 39.61 Seconds
(without alignments)
718.400 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEFIYVIT.....QTCTSTQTHKIMENKMDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	6254	100.0	1165	2	US-08-599-455B-4
2	6254	100.0	1165	4	US-09-069-781B-4
3	6246	99.9	1165	4	US-09-093-814-1
4	6246	99.9	1165	4	US-08-618-957A-11
5	6172	98.7	1165	2	US-08-640-389A-11
6	4819.5	77.1	958	4	US-08-618-957A-8
7	4819.5	77.1	960	1	US-08-355-888A-8
8	4819.5	77.1	960	2	US-08-693-697-8
9	4819.5	77.1	960	2	US-08-640-389A-3
10	4819.5	77.1	960	3	US-08-693-696-8
11	4816	77.0	960	2	US-08-588-190-3
12	4814.5	77.0	960	2	US-08-618-957A-3
13	4814.5	77.0	960	4	US-08-618-957A-10
14	4814	77.0	896	4	US-08-618-957A-36
15	4814	77.0	898	2	US-08-618-957A-9
16	4799	76.7	908	4	US-08-588-526-3
17	4791.5	76.6	958	2	US-08-640-389A-8
18	4788	76.6	906	2	US-08-640-389A-9
19	4786	76.5	896	2	US-08-640-389A-10
20	4784.5	76.5	1162	4	US-08-803-346-1
21	4776.5	76.4	1162	4	US-08-827-962-15
22	4770.5	76.3	1162	2	US-08-599-455B-43
23	4770.5	76.3	1162	4	US-08-827-962-20
24	4770.5	76.3	1162	4	US-09-069-781B-43
25	3801	60.8	896	2	US-08-640-389A-12
26	3792	60.6	894	4	US-08-618-957A-12

28	3785	60.5	894	2	US-08-599-455B-2	Sequence 2, Appl
29	3785	60.5	894	4	US-09-069-781B-2	Sequence 2, Appl
30	3779	60.4	895	4	US-08-827-962-19	Sequence 19, Appl
31	3753	60.0	895	4	US-08-827-962-21	Sequence 21, Appl
32	3057	48.9	569	1	US-08-306-231-3	Sequence 3, Appl
33	421	6.7	77	4	US-08-803-346-64	Sequence 64, Appl
34	395	6.3	76	4	US-08-803-346-61	Sequence 61, Appl
35	377	6.0	77	4	US-08-803-346-62	Sequence 62, Appl
36	370	5.9	77	4	US-08-803-346-63	Sequence 63, Appl
37	345.5	5.5	918	2	US-08-825-558-6	Sequence 6, Appl
38	316	5.1	708	1	US-07-797-556-2	Sequence 2, Appl
39	316	5.1	708	1	US-08-308-881-2	Sequence 2, Appl
40	316	5.1	708	2	US-09-058-263-2	Sequence 2, Appl
41	316	5.1	708	2	US-09-059-099-2	Sequence 2, Appl
42	316	5.1	708	3	US-09-058-264-2	Sequence 2, Appl
43	316	5.1	708	5	PCT-US95-06530-2	Sequence 2, Appl
44	313	5.0	837	1	US-07-923-976-2	Sequence 2, Appl
45	309.5	4.9	75	4	US-08-803-346-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-599-455B-4

Sequence 4, Application US/08599455B
Patent No. 5972621

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert J.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
CORRESPONDENCE ADDRESS: 44
ADDRESS: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-4

Query Match 100.0%; Score 6254; DB 2; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYITAFNLSTPITPMRFKLSGMPNSTYDYFLPAGLSKNTSNS 60
DB 1 MICOKFCVLLHWEFIYITAFNLSTPITPMRFKLSGMPNSTYDYFLPAGLSKNTSNS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANMNIOQWLKGLDLKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 180
DB 121 QOIDANMNIOQWLKGLDLKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 180
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DB 181 FQWVHCNCSVHECCCLVVPVPAKLNDTLMLCLITSGGVIFQSPIMSVQPINWVKPDP 240
QY 241 LGLHMETDDGNLKISWSSPPLVPPLQYQVKSSENSTTVIREADKIVSATSLVDSTLP 300
DB 241 LGLHMETDDGNLKISWSSPPLVPPLQYQVKSSENSTTVIREADKIVSATSLVDSTLP 300
QY 301 GSSYEVOVRGKRLDGPGLMSDSTPRVFTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEVOVRGKRLDGPGLMSDSTPRVFTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIWMNMNLAEKIPQSQYDVVDVSDHVKVTFPFLNETKPRGFTYDAYVCCNEHECHH 420
DB 361 VPSKEIWMNMNLAEKIPQSQYDVVDVSDHVKVTFPFLNETKPRGFTYDAYVCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEIDGYLTMTCRWSTSTIOSLAESTLQRLRYHRSSLYCSDIPSIH 480
DB 421 RYAEIYVIDVNINISCEIDGYLTMTCRWSTSTIOSLAESTLQRLRYHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
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DB 661 TLLMKPLMKNDSLCSYQRYVINHTSCNGTWSGVDGNHTKFTFLWTEQAHVTYLAINSI 720
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DB 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIYVSWILSPSDYKLMYFLIEWKNLNED 780
QY 781 GEIKWLRISSSVKKYYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
DB 781 GEIKWLRISSSVKKYYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
QY 841 GLYVIVPVIISSTILLGLTLLSHQRMKLFWEDEVNPNKNCWAGLNFQKPETFEHLFI 900
DB 841 GLYVIVPVIISSTILLGLTLLSHQRMKLFWEDEVNPNKNCWAGLNFQKPETFEHLFI 900
QY 901 KHTASVTCGPLEPETISEDISVDTSWKNDEMPTTVVSLSTLDLEKGSVCISDOFN 960
DB 901 KHTASVTCGPLEPETISEDISVDTSWKNDEMPTTVVSLSTLDLEKGSVCISDOFN 960

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QY 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1080
DB 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLODSCHFVENNINIGTSSKKTFFAS 1140
DB 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLODSCHFVENNINIGTSSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 2

US-09-069-781B-4

Sequence 4, Application US/09069781B

Patent No. 6287782

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,781B

FILING DATE: 29-APRIL-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/864,564

FILING DATE: 28-MAY-1997

APPLICATION NUMBER: US 08/708,123

FILING DATE: 03-SEP-1996

APPLICATION NUMBER: US 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: US 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: US 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: US 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: US 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: US 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: US 08/562,663

FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Melkielejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/082001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-069-781B-4

Query Match 100.0%; Score 6254; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHMEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAPEPKFNSSGTHFSNLSTTFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAPEPKFNSSGTHFSNLSTTFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGLDLKLFICYVESLFEKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGLDLKLFICYVESLFEKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCLKITSGGVIFQSPILMSVQPINMVKPDP 240
Db 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCLKITSGGVIFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKLISWSSPPLVPFLQYQVYKSENSTTVIREADKIVSATSLVD 300
Db 241 LGLHMEITDDGNLKLISWSSPPLVPFLQYQVYKSENSTTVIREADKIVSATSLVD 300
QY 301 GSSYEVOVRGKRLDGPGLMSDSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKENKI 360
Db 301 GSSYEVOVRGKRLDGPGLMSDSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
QY 421 RYAEIYVIVNINISCEITDGYLTKMTCRSTSTQSLAESTLQRLRYHRSLSYCS 480
Db 421 RYAEIYVIVNINISCEITDGYLTKMTCRSTSTQSLAESTLQRLRYHRSLSYCS 480
QY 481 PISEPKDCYLDGDFEYECIFQPIFILSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPL 540
Db 481 PISEPKDCYLDGDFEYECIFQPIFILSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPL 540
QY 541 SSVKAEITINIGLKLISWEKVPFPENNLFQIRYGLSGKEVQMKMEYVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKLISWEKVPFPENNLFQIRYGLSGKEVQMKMEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGDPFWRILINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGDPFWRILINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHVTVALINSI 720
Db 661 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHVTVALINSI 720
QY 721 GASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIYSWILSPSDYKLMYFIIEWKMLNED 780
Db 721 GASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIYSWILSPSDYKLMYFIIEWKMLNED 780
QY 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIEMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIEMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVIVPIISSSILLLGLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFQKPEFTEHLEFI 900
Db 841 GLYIVIVPIISSSILLLGLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFQKPEFTEHLEFI 900

QY 901 KHTASVTCGPLLLEPETISEDISVTSWKNKDEMPITVSVLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVTSWKNKDEMPITVSVLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEAEGETEVTYEDESORQPFVKYATLISNSKPSSETGEEQGLINSSVCKCSSKNSPL 1020
Db 961 SVNFSEAEGETEVTYEDESORQPFVKYATLISNSKPSSETGEEQGLINSSVCKCSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTSEGLDELKLEGNFPENNNDKKSIIYL 1080
Db 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTSEGLDELKLEGNFPENNNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINUGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINUGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 3

US-09-093-814-1
Sequence 1, Application US/09093814
Patent No. 6270981
GENERAL INFORMATION:
APPLICANT: Carpenter et al.
TITLE OF INVENTION: ASSAY SYSTEMS FOR LEPTIN-ENHANCING AGENTS
FILE REFERENCE: REG 580-A
CURRENT APPLICATION NUMBER: US/09/093,814
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/049,108
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-093-814-1

Query Match 99.9%; Score 6246; DB 4; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHMEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAPEPKFNSSGTHFSNLSTTFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAPEPKFNSSGTHFSNLSTTFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGLDLKLFICYVESLFEKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGLDLKLFICYVESLFEKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCLKITSGGVIFQSPILMSVQPINMVKPDP 240
Db 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCLKITSGGVIFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKLISWSSPPLVPFLQYQVYKSENSTTVIREADKIVSATSLVD 300
Db 241 LGLHMEITDDGNLKLISWSSPPLVPFLQYQVYKSENSTTVIREADKIVSATSLVD 300
QY 301 GSSYEVOVRGKRLDGPGLMSDSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKENKI 360
Db 301 GSSYEVOVRGKRLDGPGLMSDSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420

QY 421 RYAEIYIDVNNINISCEITDGYLTGKMTCRMSTSTIOSLAESTLOLRHRSLSYCSDIPSIH 480
DB 421 RYAEIYIDVNNINISCEITDGYLTGKMTCRMSTSTIOSLAESTLOLRHRSLSYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
DB 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEYQWKMEYVDKAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEYQWKMEYVDKAKSKSVSLPV 600
QY 601 PDLCAVYAVOYRCKRLDGLGYSWNSNPAITVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVOYRCKRLDGLGYSWNSNPAITVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDLSLVQRYVINHHTSCNGTSEEDVGNHTKFTFLMTEQAHTVTLAINSI 720
DB 661 TLLWKPLMKNDLSLVQRYVINHHTSCNGTSEEDVGNHTKFTFLMTEQAHTVTLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIVQSLAAYPLNSSCVIVSWILSPSDYKIMYFIEMKNLNE 780
DB 721 GASVANFNLTFSWPMKSVNIVQSLAAYPLNSSCVIVSWILSPSDYKIMYFIEMKNLNE 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFHEHFI 900
DB 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFHEHFI 900
QY 901 KHTASVTCGPILEPETISEDISVDTSKKNKDEMPPTVSVSLSTDLEKGSVCISDOFN 960
DB 901 KHTASVTCGPILEPETISEDISVDTSKKNKDEMPPTVSVSLSTDLEKGSVCISDOFN 960
QY 961 SVNFSEAEGETEYDESOQOPFVKIATLLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
DB 961 SVNFSEAEGETEYDESOQOPFVKIATLLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTSEGLDELKLEGNPPEENNDDKSIYYL 1080
DB 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTSEGLDELKLEGNPPEENNDDKSIYYL 1080
QY 1081 GVTSIKKRESGYLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
DB 1081 GVTSIKKRESGYLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 4
US-08-618-957A-11
: Sequence 11, Application us/08618957A
: Patent No. 6355237
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. Ralph
: APPLICANT: Cioffici, Joseph
: APPLICANT: Zupancic, Thomas Joel
: APPLICANT: Shafer, Alan Wayne
: TITLE OF INVENTION: METHODS FOR USING THE OBES
: TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of The Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA

ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-11

Query Match 99.9%; Score 6246; DB 4; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCYVLLHWEFIYVITAENLSYPTTPWRFKLSKMPNNTYDYFLLPAGLSKNTS 60
DB 1 MICQKFCYVLLHWEFIYVITAENLSYPTTPWRFKLSKMPNNTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCISLADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCISLADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNNIQWLKGLDKLFICYVESLFLKLFNRYNYKVHLLVYLPVLEDSPLVPQKS 180
DB 121 QOIDANNNIQWLKGLDKLFICYVESLFLKLFNRYNYKVHLLVYLPVLEDSPLVPQKS 180
QY 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPPLMSVQPINMVKPDP 240
DB 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPPLMSVQPINMVKPDP 240
QY 241 LGLHMETDDGNLKISWSSPLVPFLQYQVYKSENSTTVIREADKIVATSLSLVDSILP 300
DB 241 LGLHMETDDGNLKISWSSPLVPFLQYQVYKSENSTTVIREADKIVATSLSLVDSILP 300
QY 301 GSSYEYQVYRGKRLDGPGLMSDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEYQVYRGKRLDGPGLMSDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIYWMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYWMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYIDVNNINISCEITDGYLTGKMTCRMSTSTIOSLAESTLOLRHRSLSYCSDIPSIH 480
DB 421 RYAEIYIDVNNINISCEITDGYLTGKMTCRMSTSTIOSLAESTLOLRHRSLSYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
DB 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEYQWKMEYVDKAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEYQWKMEYVDKAKSKSVSLPV 600

Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSMNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYSWNSMNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSESDVGNHTKFTPLMTEQAHTVTLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSESDVGNHTKFTPLMTEQAHTVTLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
QY 781 GEIKMLRISSSVKYYIHDHFIPLEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKYYIHDHFIPLEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDVNPKNCSMAOGLNFQKPEFHEHLEFI 900
Db 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDVNPKNCSMAOGLNFQKPEFHEHLEFI 900
QY 901 KHTASVTCGPLLEPETISEDIVDSWKNKDEMPPTVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLEPETISEDIVDSWKNKDEMPPTVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEAEGETEVTYEAESQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETEVTYEAESQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSSNSWEIEAOAFILSDQHPNITSPHLTFSEGLDELKLEGNPPEENNDDKSIYYL 1080
Db 1021 KDSFSSNSWEIEAOAFILSDQHPNITSPHLTFSEGLDELKLEGNPPEENNDDKSIYYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCUFTDIRVLQDSCHFEVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCUFTDIRVLQDSCHFEVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 5
US-08-640-389A-11
; Sequence 11, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-640-389A-11

Query Match 98.7%; Score 6172; DB 2; Length 1165;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1155; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

QY 1 MICQRCVYLLHWEFIYVITAFNLSYPIPTWRFKLSMPNSTYDYFLPAGLSKNTSNS 60
Db 1 MICQRCVYLLHWEFIYVITAFNLSYPIPTWRFKLSMPNSTYDYFLPAGLSKNTSNS 60
QY 61 NGHYETAPEPKFNSSGTHFNSLSKTFHCCFRSEODRNCISLADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAPEPKFNSSGTHFNSLSKTFHCCFRSEODRNCISLADNIEGTFVSTVNSLVF 120
QY 121 QOIDANNIQCWLKGLDKLFICYVESLFRNRYNYKVHLLVLPVLEDSPLVPQGS 180
Db 121 QOIDANNIQCWLKGLDKLFICYVESLFRNRYNYKVHLLVLPVLEDSPLVPQGS 180
QY 181 FQNVHCNSVHECCCLVPPTAKLNDTLLMCLKITSGVITFQSPILMSVQPINMVKPDP 240
Db 181 FQNVHCNSVHECCCLVPPTAKLNDTLLMCLKITSGVITFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMETDDGNLKISWSSPLVPFPLOQVKKSENSTVIREADKIVATSLLVDSILP 300
Db 241 LGLHMETDDGNLKISWSSPLVPFPLOQVKKSENSTVIREADKIVATSLLVDSILP 300
QY 301 GSSYEVOYRGKRLDGPIMSDWSTPRVFTTQDYIYFPFKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEVOYRGKRLDGPIMSDWSTPRVFTTQDYIYFPFKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIWMNMNLAEKIPQSOYDVVSDHVSQVTFNLETKPRGFTYDAVYCCNEHECHH 420
Db 361 VPSKEIWMNMNLAEKIPQSOYDVVSDHVSQVTFNLETKPRGFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNNINISCESTDGYLTCKMTCRSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480
Db 421 RYAEIYVIDVNNINISCESTDGYLTCKMTCRSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSMNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYSWNSMNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSESDVGNHTKFTPLMTEQAHTVTLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSESDVGNHTKFTPLMTEQAHTVTLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780

QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHORMKLLFWEDEVNPNKNCSWAQLNFORPEFHELF1 900
Db 841 GLYVIVPVISSSILLGLTLLISHORMKLLFWEDEVNPNKNCSWAQLNFORPEFHELF1 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKKNDEKMPPTVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLEPETISEDISVDTSMKKNDEKMPPTVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFEAEGETEVTYEDESQROPFVKYATLISNSKRPSETGEEGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFEAEGETEVTYEDESQROPFVKYATLISNSKRPSETGEEGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYLL 1080
Db 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYLL 1080
QY 1081 GVTSIKKRESGYLLTDKSRVSCFPAPCLFTDIRVLQDSCHFEVENNINIGTSSKKTPEAS 1140
Db 1081 GVTSIKKRESGYLLTDKSRVSCFPAPCLFTDIRVLQDSCHFEVENNINIGTSSKKTPEAS 1140
QY 1141 YMPQFOTCSTQ-THKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQ-THKIME-KMCDLTV 1165

RESULT 6

US-08-618-957A-8
; Sequence 8, Application US/08618957A
; Patent No. 6355237

GENERAL INFORMATION:

APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBES
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 958 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-8

Query Match 77.1%; Score 4819.5; DB 4; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVVLHMEFIYVITAFNLSTPIPTPRFKLSCMPNSTYDYFLPAGLSKNTSNS 60
Db 1 MICQKFCVVLHMEFIYVITAFNLSTPIPTPRFKLSCMPNSTYDYFLPAGLSKNTSNS 60
QY 61 NGHYETAVERKFNSSGTHFSNLSKTYFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVERKFNSSGTHFSNLSKATFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNIOCNLKGDKLFICYVESLEFKNLEFRNYNKVHLLVLPPEVLEDSPLVPQKGS 180
Db 121 QOIDANWNIOCNLKGDKLFICYVESLEFKNLEFRNYNKVHLLVLPPEVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMCLKITSGVIFQSPILMSVQPINMVKPDP 240
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMCLKITSGVIFERSPLMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOYQVYSENSTTVIREADKIVATSLLVDLILP 300
Db 241 LGLHMEITDDGNLKSWSPPPLVPFPLOYQVYSENSTTVIREADKIVATSLLVDLILP 300
QY 301 GSSYEQVGRKRLDGPGLWSDMSTPRVFTQDVLYFPPKILTSVGSNVSFHCYKKEKNI 360
Db 301 GSSYEQVGRKRLDGPGLWSDMSTPRVFTQDVLYFPPKILTSVGSNVSFHCYKKEKNI 360
QY 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVFPENLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVFPENLNETKPRGKFTYDAVYCCNEHECH 420
QY 421 RYAEIYVIDVININISCEITDGYLTAKMTCRNSTSTIOSLAESTLQLRHSSLYCSDIPS 480
Db 421 RYAEIYVIDVININISCEITDGYLTAKMTCRNSTSTIOSLAESTLQLRHSSLYCSDIPS 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGTYMIRINHSLSGLSDSPRCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGTYMIRINHSLSGLSDSPRCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKLISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKLISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTBOAHTVTLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTBOAHTVTLAINSI 720
QY 721 GASVANFNLTFSWPMNSKVINIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 721 GASVANFNLTFSWPMNSKVINIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHORMKLLFWEDEVNPNKNCSWAQLNFORPEFHELF1 900
Db 841 GLYVIVPVISSSILLGLTLLISHORMKLLFWEDEVNPNKNCSWAQLNFORPEFHELF1 900
QY 894 TFEHLFIKHT-ASVTCGP-----LLLEPETISEDISVDTSMKKNDE 933
Db 901 SHHSLISSYQGHKHGCRPGPLHRRKTRDCLSLVLLTLPPLLSYDPAKSPSVRNTQ 958

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RESULT 7
US-08-355-888A-8
; Sequence 8, Application US/08355888A
; Patent No. 5763211
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,888A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-355-888A-8

Query Match          77.1%; Score 4819.5; DB 1; length 960;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;
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Db 303 GSSYEYQVGRKRLDGPGLMSDWSPTPRVFTTQDVYTFPPKILTSVGSNVSFHCYKKENKI 362
QY 361 VPSKEIVMMNMLAEKIPQSQYDVVSDHVSQVTEFNLNETKPRGKFTYDAVCCNEHECHH 420
Db 363 VPSKEIVMMNMLAEKIPQSQYDVVSDHVSQVTEFNLNETKPRGKFTYDAVCCNEHECHH 422
QY 421 RYAEIYIDVININISCESTDGYLTFTKMTGWSSTIQSLAESTLQLRHRSLSYCSIDPSIH 480
Db 423 RYAEIYIDVININISCESTDGYLTFTKMTGWSSTIQSLAESTLQLRHRSLSYCSIDPSIH 482
QY 481 PISEPKDCYQSDGEYECIFQPIFLSGYTMIRINSHLSGLSDSPPTCYLPDSVVKPLPP 540
Db 483 PISEPKDCYQSDGEYECIFQPIFLSGYTMIRINSHLSGLSDSPPTCYLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQWMEYVDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQWMEYVDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVGRKRLDGLGYSNWSNPAVTVMDIKVPMRGPEFWRIRINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVGRKRLDGLGYSNWSNPAVTVMDIKVPMRGPEFWRIRINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSQSDVGNHTKFTPLMTQAHVTVLAINSI 720
Db 663 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSQSDVGNHTKFTPLMTQAHVTVLAINSI 722
QY 721 GASVANENLTFSWPMKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 723 GASVANENLTFSWPMKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 782
QY 781 GEIKWLRISSSVKYYIHDFIPIEKYQESLYPIFMEGVGPKKINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSSVKYYIHDFIPIEKYQESLYPIFMEGVGPKKINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVITSSILLTLLISHQRMKLFMEDVPPNPKNCWAGLNFQK-----PE 893
Db 843 GLYVIVPVITSSILLTLLISHQRMKLFMEDVPPNPKNCWAGLNFQKLEGSMEFK 902
QY 894 TFEHLFIKHT-ASVTGCP-----LLLEPETISEDTSVDTSWKNKDE 933
Db 903 SHHSLISSIQGHKHGCRPQGPLHRTKTRDLSLVYLLTLPPLSLSTPAKSPSVRNTQE 960

RESULT 8
US-08-693-697-8
; Sequence 8, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
```

REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-697-8

Query Match 77.1%; Score 4819.5; DB 2; Length 960;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVVLHWEFIYVITAFNLSTPTPWREKLSGMPNSTYDYFLLPAGLSKNTS 60
DB 3 MICQKFCVVLHWEFIYVITAFNLSTPTPWREKLSGMPNSTYDYFLLPAGLSKNTS 62
QY 61 NGHYETAEPKFNSSGTHFSNLSTPTWREKLSGMPNSTYDYFLLPAGLSKNTS 120
DB 63 NGHYETAEPKFNSSGTHFSNLSTPTWREKLSGMPNSTYDYFLLPAGLSKNTS 122
QY 121 QOIDANWNIQWLKGLDKLFICYVESLFRNLFRNYKVHLLVLEPEVLEDSPLVPQKS 180
DB 123 QOIDANWNIQWLKGLDKLFICYVESLFRNLFRNYKVHLLVLEPEVLEDSPLVPQKS 182
QY 181 FQMVHNCVSHECCCECLVPPTAKLNDLMLCLKITSQGVIFQSPILMSVQPINMKPDP 240
DB 183 FQMVHNCVSHECCCECLVPPTAKLNDLMLCLKITSQGVIFQSPILMSVQPINMKPDP 242
QY 241 LGLHMETDGNLKISWSSPPLVPPLQYQVYSENSTVIREADKIVSATSLVDSTLP 300
DB 243 LGLHMETDGNLKISWSSPPLVPPLQYQVYSENSTVIREADKIVSATSLVDSTLP 302
QY 301 GSSYEVOVGRKRLDGPGLMSDWSPTPRVFTQDVLYFPKILTSVGSNVSFHCITYKKNKI 360
DB 303 GSSYEVOVGRKRLDGPGLMSDWSPTPRVFTQDVLYFPKILTSVGSNVSFHCITYKKNKI 362
QY 361 VPSKEIVMMNLAEKIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
DB 363 VPSKEIVMMNLAEKIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 422
QY 421 RYAEIYVIDVNNISCEITDGYLTMTKCRSTSTIOSLAESTIQLRHRSSLYCSDIPS 480
DB 423 RYAEIYVIDVNNISCEITDGYLTMTKCRSTSTIOSLAESTIQLRHRSSLYCSDIPS 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 483 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLKLISWEKPVFPENNLOQIRYGLSGKEVQWKMEYVDKAKSKSVSLPV 600
DB 543 SSVKAEITINIGLKLISWEKPVFPENNLOQIRYGLSGKEVQWKMEYVDKAKSKSVSLPV 602
QY 601 PDLCAVYAVQVGRKRLDGLGYWSNWSNPATVVMIDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 603 PDLCAVYAVQVGRKRLDGLGYWSNWSNPATVVMIDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLMKPLKNDSCSVQRYVINHTSCNGTWSSEVGNHTKFTFLMTQAHVTVLAINSI 720
DB 663 TLLMKPLKNDSCSVQRYVINHTSCNGTWSSEVGNHTKFTFLMTQAHVTVLAINSI 722
QY 721 GASVANENLTFSPMSKVNIVQSLATPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
DB 723 GASVANENLTFSPMSKVNIVQSLATPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 782
QY 781 GEIKWLRISSSVKKYIYHDFIPIEKYQPSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840

DB 783 GEIKWLRISSSVKKYIYHDFIPIEKYQPSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 842
QY 841 GLYIVIPVITSSSILLGLTLLISHQRMKLLFWEDVDPNPKNCSNAOGLNFQK-----PE 893
DB 843 GLYIVIPVITSSSILLGLTLLISHQRMKLLFWEDVDPNPKNCSNAOGLNFQKLEGSMEFYK 902
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSWKNKDE 933
DB 903 SHHSLISSTQGHKHGCRPQGPLHRRTRDLCSLVYLLTLPPLLSYDPAKSPSVRNTQE 960

RESULT 9

US-08-640-389A-3

Sequence 3, Application US/08640389A.

Patent No. 5912123

GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.

APPLICANT: Cioffi, Joseph

APPLICANT: Zupancic, Thomas J.

APPLICANT: Shafer, Alan W.

TITLE OF INVENTION: DETECTION OF THE LEPTIN

TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR

TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/640,389A

FILING DATE: 29-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 8907-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 960 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-640-389A-3

Query Match 77.1%; Score 4819.5; DB 2; Length 960;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVVLHWEFIYVITAFNLSTPTPWREKLSGMPNSTYDYFLLPAGLSKNTS 60
DB 3 MICQKFCVVLHWEFIYVITAFNLSTPTPWREKLSGMPNSTYDYFLLPAGLSKNTS 62
QY 61 NGHYETAEPKFNSSGTHFSNLSTPTWREKLSGMPNSTYDYFLLPAGLSKNTS 120
DB 63 NGHYETAEPKFNSSGTHFSNLSTPTWREKLSGMPNSTYDYFLLPAGLSKNTS 122
QY 121 QOIDANWNIQWLKGLDKLFICYVESLFRNLFRNYKVHLLVLEPEVLEDSPLVPQKS 180
DB 123 QOIDANWNIQWLKGLDKLFICYVESLFRNLFRNYKVHLLVLEPEVLEDSPLVPQKS 182


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QY 181 FQWVHCNCSVHECCCLVVPVPTAKLNDTLLMCLKITSQGVTFQSPMSVQPINMVKPPDP 240
Db 183 FQWVHCNCSVHECCCLVVPVPTAKLNDTLLMCLKITSQGVTFQSPMSVQPINMVKPPDP 242
QY 241 LGLHMEITDDGNLKSISWSSPLVPFPLOQYQVKSSENSTVIIRADKIVATSLSLVDSILP 300
Db 243 LGLHMEITDDGNLKSISWSSPLVPFPLOQYQVKSSENSTVIIRADKIVATSLSLVDSILP 302
QY 301 GSSYEVOYRGKRLDGPISWDSMTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI 360
Db 303 GSSYEVOYRGKRLDGPISWDSMTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI 362
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSSTIQLAESTLQLRHRSLSYCSIDIPSIH 480
Db 423 RYAEIYVIDVININISCEITDGYLTKMTCRWSSTIQLAESTLQLRHRSLSYCSIDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOQOIRYGLSGKEVQWKMTEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVFPENNLOQOIRYGLSGKEVQWKMTEVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSQSDVGNHTKFPFLWTEQAHVTVLAINSI 720
Db 663 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSQSDVGNHTKFPFLWTEQAHVTVLAINSI 722
QY 721 GASVANENLTFESWPMKSVNIQVOSTSAYPLNSSCVIYVSWILSPDYKLMYFLIEWKNLNED 780
Db 723 GASVANENLTFESWPMKSVNIQVOSTSAYPLNSSCVIYVSWILSPDYKLMYFLIEWKNLNED 782
QY 781 GEIKMLRISSSVKYYIHDHFIPIEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKMLRISSSVKYYIHDHFIPIEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYIYVPIIISSTILLGTLTISHORMKKLFWEDVPNPKNCMAOGLNFQKMLEGSMFVK 902
Db 843 GLYIYVPIIISSTILLGTLTISHORMKKLFWEDVPNPKNCMAOGLNFQKMLEGSMFVK 902
QY 894 TPEHLEFIKHT-ASVTCGP-----LLEPETISEDISVDTSWKNKDE 933
Db 903 SHHSLISTQGHKHCGRPGQPLHRTKTRDCLSLVYLLTLPPLSYDPAKSPSVRNTQE 960

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RESULT 10
US-08-693-696-8
; Sequence 8, Application US/08693696
; Patent No. 6005080
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1 219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,888
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-693-696-8

Query Match 77.1%; Score 4819.5; DB 3; Length 960;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTYPTPWRFKLSQMPNPNSTYDFLLPAGLSKNTSNS 60
Db 3 MICQKFCVLLHMEFIYVITAFNLSTYPTPWRFKLSQMPNPNSTYDFLLPAGLSKNTSNS 62
QY 61 NGHYETAVEERKFNSSGTHFSNLSTKTHCCFRSEODRNCISLADNIEGKTFVSTVNSLYF 120
Db 63 NGHYETAVEERKFNSSGTHFSNLSTKTHCCFRSEODRNCISLADNIEGKTFVSTVNSLYF 122
QY 121 QQIDANNIQCWLKGDCLKFLICYVESLEKFLFRNRYKVVHLLVLPBEVLDSPLVPQKGS 180
Db 123 QQIDANNIQCWLKGDCLKFLICYVESLEKFLFRNRYKVVHLLVLPBEVLDSPLVPQKGS 182
QY 181 FQWVHCNCSVHECCCLVVPVPTAKLNDTLLMCLKITSQGVTFQSPMSVQPINMVKPPDP 240
Db 183 FQWVHCNCSVHECCCLVVPVPTAKLNDTLLMCLKITSQGVTFQSPMSVQPINMVKPPDP 242
QY 241 LGLHMEITDDGNLKSISWSSPLVPFPLOQYQVKSSENSTVIIRADKIVATSLSLVDSILP 300
Db 243 LGLHMEITDDGNLKSISWSSPLVPFPLOQYQVKSSENSTVIIRADKIVATSLSLVDSILP 302
QY 301 GSSYEVOYRGKRLDGPISWDSMTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI 360
Db 303 GSSYEVOYRGKRLDGPISWDSMTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI 362
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSSTIQLAESTLQLRHRSLSYCSIDIPSIH 480
Db 423 RYAEIYVIDVININISCEITDGYLTKMTCRWSSTIQLAESTLQLRHRSLSYCSIDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOQOIRYGLSGKEVQWKMTEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVFPENNLOQOIRYGLSGKEVQWKMTEVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

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|||||
Db 603 PDLCAVYAVQYRCKRLDGLGWSNWSNPAYTVVMDIKVPMRGPEFWRLINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 663 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 723 GASVANFNLTFSWPMMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 782
QY 781 GEIKWLRISSSVKYYIHDHFPIEIKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSSVKYYIHDHFPIEIKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYIVPVIITSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQK-----PE 893
Db 843 GLYIVPVIITSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKMLEGSMFVK 902
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSWKNKDE 933
Db 903 SHHSLISTQGHKHCGRPOGPLHRKTRDLCSLVYLLTLPPLLSYDPAKSPSVRNTQOE 960

RESULT 11
US-08-693-697-33

; Sequence 33, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffili, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-693-697-33

Query Match 77.0%; Score 4816; DB 2; Length 908;
Best Local Similarity 99.1%; Pred. No. 0;

Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
QY 1 MICQKECVLLHWEFIYVITAFNLSTPTPWRFKLSCMPNNTYDYFLLPAGLSKNTSNS 60
Db 3 MICQKECVLLHWEFIYVITAFNLSTPTPWRFKLSCMPNNTYDYFLLPAGLSKNTSNS 62
QY 61 NGHYETAVERPENSSGTHFSNLKSTPHCCFRSEQDRNCSLCAADNIEGKTFVSTVNSLVF 120
Db 63 NGHYETAVERPENSSGTHFSNLKSTPHCCFRSEQDRNCSLCAADNIEGKTFVSTVNSLVF 122
QY 121 QOIDANMNIQCMLEKDKLFICYVESLEFKNLFRNRYKVHLLYVLEPLEDSPLVPQKGS 180
Db 123 QOIDANMNIQCMLEKDKLFICYVESLEFKNLFRNRYKVHLLYVLEPLEDSPLVPQKGS 182
QY 181 FQMVHCNCSYHECCECLVPVPTAKLNDTLLMCLKITSGGVIIFQSPINMSVQPINMVKPDP 240
Db 183 FQMVHCNCSYHECCECLVPVPTAKLNDTLLMCLKITSGGVIIFQSPINMSVQPINMVKPDP 242
QY 241 LGLHMETDDGNLKISWSSPPLVPFLOYQVYKSENSTVIREADKIYATSLLVDSILP 300
Db 243 LGLHMETDDGNLKISWSSPPLVPFLOYQVYKSENSTVIREADKIYATSLLVDSILP 302
QY 301 GSSYEVOYRGRKRLDGPISWSDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 303 GSSYEVOYRGRKRLDGPISWSDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 362
QY 361 VPSKEIYWMNLAEKIPQSOYDVVSDHVSQVTFNLTETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYWMNLAEKIPQSOYDVVSDHVSQVTFNLTETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480
Db 423 RYAEIYVIDVNIINISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 482
QY 481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITTINGLKLISWEKPVFPENNLOQIRYGLSGKEVQWKYEVYDAKSKSVSLPV 600
Db 543 SSVKAEITTINGLKLISWEKPVFPENNLOQIRYGLSGKEVQWKYEVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQYRCKRLDGLGWSNWSNPAYTVVMDIKVPMRGPEFWRLINGDTMKKEKNV 660
Db 603 PDLCAVYAVQYRCKRLDGLGWSNWSNPAYTVVMDIKVPMRGPEFWRLINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 663 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 723 GASVANFNLTFSWPMMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 782
QY 781 GEIKWLRISSSVKYYIHDHFPIEIKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSSVKYYIHDHFPIEIKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYIVPVIITSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQK-----PETFEHL 898
Db 843 GLYIVPVIITSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKMPGTKELL 902

RESULT 12
US-08-588-190-3

; Sequence 3, Application US/08588190
; Patent No. 5856098
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cioffili, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR

;; TITLE OF INVENTION: VARIANT AND METHODS FOR REGULATING OBESITY
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2811
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/588,190
;; FILING DATE: 18-JAN-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Polissant, Brian M.
;; REGISTRATION NUMBER: 28,462
;; REFERENCE/DOCKET NUMBER: 008907-0029-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-493-4935
;; TELEFAX: 650-493-5556
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 960 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-588-190-3

Query Match 77.0%; Score 4814.5; DB 2; Length 960;
Best local Similarity 93.9%; Pred. No. 0;
Matches 900; Conservative 7; Mismatches 26; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHWEFIYVITAFNISYPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60
|||
Db 3 MICQKFCVLLHWEFIYVITAFNISYPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 62

QY 61 NGHYETAVERKFNSSGTHFSNLSKTEFHCCFRSEQDRNCSICADNIEGKTFVSTVNSLVF 120
|||
Db 63 NGHYETAVERKFNSSGTHFSNLSKTEFHCCFRSEQDRNCSICADNIEGKTFVSTVNSLVF 122

QY 121 QOIDANWNIIQCMWKGLDKLFICVESLFRNLFNRYNKVHLLVYLPEVLEDSPLVPQKGS 180
|||
Db 123 QOIDANWNIIQCMWKGLDKLFICVESLFRNLFNRYNKVHLLVYLPEVLEDSPLVPQKGS 182

QY 181 FQVYHNCVSVHECCCLVPVPYPAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240
|||
Db 183 FQVYHNCVSVHECCCLVPVPYPAKLNDTLLMCLKITSQGVIFRSPILMSVQPINMVKPDP 242

QY 241 LGLHMEITDDGNLKISWSSPPLVPFLOQYQVYSENSTTVIREADKIVSATSLVDLSILP 300
|||
Db 243 LGLHMEITDDGNLKISWSSPPLVPFLOQYQVYSENSTTVIREADKIVSATSLVDLSILP 302

QY 301 GSSYEYQVRGKRLDGPGLWSDWSPRVTQDVYFPPKILTSVGSNVSFHCYKKENKI 360
|||
Db 303 GSSYEYQVRGKRLDGPGLWSDWSPRVTQDVYFPPKILTSVGSNVSFHCYKKENKI 362

QY 361 VPSKEIYVMMNLAEKIPQSQDYVSDHVSQVTFNLTETKPRCKFTYDAVYCCNEHECHH 420
|||
Db 363 VPSKEIYVMMNLAEKIPQSQDYVSDHVSQVTFNLTETKPRCKFTYDAVYCCNEHECHH 422

QY 421 RYAEIYVIDVININISCETDGYLTMTCTRWSTSTIOSLAESTLOLRHRSLLYCSIDIPSIH 480
|||

Db 423 RYAEIYVIDVININISCETDGYLTMTCTRWSTSTIOSLAESTLOLRHRSLLYCSIDIPSIH 482

QY 481 PISEPKDCYLOSDFEYECIFQPIFLISGYTMIRINSHLSGLDSPPTCVLPDSVVKPLPP 540
|||
Db 483 PISEPKDCYLOSDFEYECIFQPIFLISGYTMIRINSHLSGLDSPPTCVLPDSVVKPLPP 542

QY 541 SSVKAEITINIGLTKISWEKVPFPPENNLQFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
|||
Db 543 SSVKAEITINIGLTKISWEKVPFPPENNLQFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 602

QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 660
|||
Db 603 PDLCAVYAVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 662

QY 661 TLMKPLMKNDLSLSVQRYVINHHTSCNGTWSQEDVGNHTKFTFLMTEQAHTVTLAINSI 720
|||
Db 663 TLMKPLMKNDLSLSVQRYVINHHTSCNGTWSQEDVGNHTKFTFLMTEQAHTVTLAINSI 722

QY 721 GASVANFNLTFSWPMMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKIMYFIIEWKNLNE 780
|||
Db 723 GASVANFNLTFSWPMMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKIMYFIIEWKNLNE 782

QY 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
|||
Db 783 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842

QY 841 GLYIVPVYIISSSILLGLTLISHQRMKLLFWEDVPNPKNCNMAQGLNFQK-----PE 893
|||
Db 843 GLYIVPVYIISSSILLGLTLISHQRMKLLFWEDVPNPKNCNMAQGLNFQKLEGSMPVK 902

QY 894 TFEHLPIKHT-ASVTCGP-----LLEPETISEDISVDTSMKNKDE 933
|||
Db 903 SHHSLISSTQGHKHCGRPQGRPLHRKTRDLSLVYLLTLPPLLSYDPAKSPSVRNTQE 960

RESULT 13
US-08-618-957A-3
; Sequence 3, Application US/08618957A
; Patent No. 6355237
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: CIOFFI, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: METHODS FOR USING THE OBSE
; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,957A
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Polissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 008907-0033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-3

Query Match 77.0%; Score 4814.5; DB 4; Length 960;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 900; Conservative 7; Mismatches 26; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHMEFIYVITAFNLSYPTTPMRKLSCMPNSTYDYFLPAGLSKNTSNS 60
DB 3 MICQKFCVLLHMEFIYVITAFNLSYPTTPMRKLSCMPNSTYDYFLPAGLSKNTSNS 62
QY 61 NGHYETAVERPKNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
DB 63 NGHYETAVERPKNSSGTHFSNLSKATFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 122
QY 121 QOIDANWNIQCWLKGDCLKFICYVESLFKNLFRNRYKVHLLYLPEVLEDSPLVPQKGS 180
DB 123 QOIDANWNIQCWLKGDCLKFICYVESLFKNLFRNRYKVHLLYLPEVLEDSPLVPQKGS 182
QY 181 FQMVHCNCSVHECECLVPVPTAKLNDTLNCLKITSQGVIFOSPLMSYQPINMVKPDPP 240
DB 183 FQMVHCNCSVHECECLVPVPTAKLNDTLNCLKITSQGVIFRSPLMSYQPINMVKPDPP 242
QY 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOYQVYSENSTTVIREADKIYSAFSLVDSILP 300
DB 243 LGLHMEITDDGNLKSISWSSPPLVPFPLOYQVYSENSTTVIREADKIYSAFSLVDSILP 302
QY 301 GSSYEVOVRGKRDLGPGIWSMDSTPRVFTQDYIYFPPKILTSVGSNVSFHCTYKKENKI 360
DB 303 GSSYEVOVRGKRDLGPGIWSMDSTPRVFTQDYIYFPPKILTSVGSNVSFHCTYKKENKI 362
QY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVFFNLNETKPRGKFTYDAVYCCNEHECHH 420
DB 363 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVFFNLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCEITDGYLTMTKCRWSTSTIQLAESTLQLRYHRSSLYCSDIPSIH 480
DB 423 RYAEIYVIDVNIINISCEITDGYLTMTKCRWSTSTIQLAESTLQLRYHRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLRP 540
DB 483 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLRP 542
QY 541 SSVKAEITINIGLKISWEKRVFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
DB 543 SSVKAEITINIGLKISWEKRVFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 602
QY 601 PDLCAVYAVOVRGKRDLGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 603 PDLCAVYAVOVRGKRDLGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTMSDEVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 663 TLLMKPLMKNDSLCSVQRYVINHTSCNGTMSDEVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSVNIVOSLSAYPLNSCIVVSWILSPSDYKLMYFLIEWKNLNE 780
DB 723 GASVANFNLTFSWPMKSVNIVOSLSAYPLNSCIVVSWILSPSDYKLMYFLIEWKNLNE 782
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSIYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 783 GEIKWLRISSSVKRYIHDHFIPIEKYQFSIYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKLFMEDVVPNPKNCSWAQGLNFQK-----PE 893

|||||
DB 843 GLYVIVPVIISSSILLGLTLLISHQRMKLFMEDVVPNPKNCSWAQGLNFQKLEGSMPVK 902
QY 894 TFEHLFIKHT-ASVTCG-----LLEPETISEDIVDTSMKNKDE 933
DB 903 SHHSLISSTGHHKGRGPRQGPLHRKTRDLSLYLLTLPPLLSYDPAKSPSVANTQE 960

RESULT 14
US-08-618-957A-10
Sequence 10, Application US/08618957A
Patent No. 6355237

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBES
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618, 957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-10

Query Match 77.0%; Score 4814; DB 4; Length 896;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSYPTTPMRKLSCMPNSTYDYFLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHMEFIYVITAFNLSYPTTPMRKLSCMPNSTYDYFLPAGLSKNTSNS 60
QY 61 NGHYETAVERPKNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
DB 61 NGHYETAVERPKNSSGTHFSNLSKATFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
QY 121 QOIDANWNIQCWLKGDCLKFICYVESLFKNLFRNRYKVHLLYLPEVLEDSPLVPQKGS 180
DB 121 QOIDANWNIQCWLKGDCLKFICYVESLFKNLFRNRYKVHLLYLPEVLEDSPLVPQKGS 180

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QY 181 FQWVHCNSVHECCCLVPPVPAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240
    |||||||
Db 181 FQWVHCNSVHECCCLVPPVPAKLNDTLLMCLKITSQGVIFRSPILMSVQPINMVKPDP 240
QY 241 LGLHMETDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLYDSILP 300
    |||||||
Db 241 LGLHMETDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLYDSILP 300
QY 301 GSSYEVOVRGKRLDGPGLMSDMSPTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
    |||||||
Db 301 GSSYEVOVRGKRLDGPGLMSDMSPTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIVMMNLAEKIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
    |||||||
Db 361 VPSKEIVMMNLAEKIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEETDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480
    |||||||
Db 421 RYAEIYVIDVNINISCEETDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFYEICIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
    |||||||
Db 481 PISEPKDCYLOSDGFYEICIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
    |||||||
Db 541 SSVKAEITINIGLKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPFEWRIINGDTMKKEKNV 660
    |||||||
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPFEWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVALAINSI 720
    |||||||
Db 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVALAINSI 720
QY 721 GASVANFNLFSPWPMKSNVQSLAYPLNSSCVIYVWILSPSDYKLMYFIIEMKLNED 780
    |||||||
Db 721 GASVANFNLFSPWPMKSNVQSLAYPLNSSCVIYVWILSPSDYKLMYFIIEMKLNED 780
QY 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
    |||||||
Db 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
QY 841 GLVYIVPVISSSILLGLTLLISHQRMKLFMEDVPPNPKNCWSAQGLNFQK 891
    |||||||
Db 841 GLVYIVPVISSSILLGLTLLISHQRMKLFMEDVPPNPKNCWSAQGLNFQK 891

RESULT 15
US-08-693-697-36
; Sequence 36, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-693-697-36

Query Match      77.0%; Score 4814; DB 2; length 898;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQFCVLLHWEFIYVITAFNISYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTS 60
    |||||||
Db 3 MICQFCVLLHWEFIYVITAFNISYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTS 62
QY 61 NGHYETAPEPKFNSSGTHFSNLKTPHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVP 120
    |||||||
Db 63 NGHYETAPEPKFNSSGTHFSNLKATFHCCFRSEQDRNCSLCADNIEGRTEFVSTVNSLVP 122
QY 121 QQIDANNIQCWLKGDCLKFICVYVSLFKNLFERNYNYKHLLVYLPEVLEDSPLVPQKS 180
    |||||||
Db 123 QQIDANNIQCWLKGDCLKFICVYVSLFKNLFERNYNYKHLLVYLPEVLEDSPLVPQKS 182
QY 181 FQWVHCNSVHECCCLVPPVPAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240
    |||||||
Db 183 FQWVHCNSVHECCCLVPPVPAKLNDTLLMCLKITSQGVIFRSPILMSVQPINMVKPDP 242
QY 241 LGLHMETDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLYDSILP 300
    |||||||
Db 243 LGLHMETDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLYDSILP 302
QY 301 GSSYEVOVRGKRLDGPGLMSDMSPTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
    |||||||
Db 303 GSSYEVOVRGKRLDGPGLMSDMSPTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 362
QY 361 VPSKEIVMMNLAEKIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
    |||||||
Db 363 VPSKEIVMMNLAEKIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNINISCEETDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480
    |||||||
Db 423 RYAEIYVIDVNINISCEETDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 482
QY 481 PISEPKDCYLOSDGFYEICIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
    |||||||
Db 483 PISEPKDCYLOSDGFYEICIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
    |||||||
Db 543 SSVKAEITINIGLKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPFEWRIINGDTMKKEKNV 660
    |||||||
Db 603 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPFEWRIINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVALAINSI 720
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DB 663 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSERVEDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANENLTFSPWPMKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFIIEMKNLNE 780
DB 723 GASVANENLTFSPWPMKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFIIEMKNLNE 782
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 783 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVIISSILLGLTLISHQRMKLFMEDVPNPKNCSWAOGLNFOK 891
DB 843 GLYVIVPVIISSILLGLTLISHQRMKLFMEDVPNPKNCSWAOGLNFOK 893

Search completed: August 15, 2002, 16:22:13
Job time: 423 sec

DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=LIVER;	
RX	MEDLINE=96206286; PubMed=8616721;	
RA	Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,	
RA	Platika D., Snodgrass H.R.;	
RT	"Novel B219/OB receptor isoforms: possible role of leptin in	
RT	hematopoiesis and reproduction.";	
RL	Nat. Med. 2:585-589(1996).	
DR	EMBL; U52914; AAC50511.1; -.	
DR	HSSP; P16471; 1BP3.	
DR	InterPro; IPR002996; CRLA.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR003529; Hematopo_receptor_L_F2.	
DR	InterPro; IPR003531; Hematopo_receptor_S_F1.	
DR	Pfam; PF00041; fn3; 2.	
DR	SMART; SM00060; FN3; 1.	
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.	
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.	
KW	Signal; Receptor.	
FT	SIGNAL	1 21 POTENTIAL.
FT	CHAIN	22 896 B219/OB RECEPTOR ISOFORM HUB219.3.
SQ	SEQUENCE	896 AA; 102516 MW; 73c431f8c578cd07 CRC64;
Query Match 77.0%; Score 4814; DB 4; Length 896;		
Best Local Similarity 99.7%; Pred. No. 0;		
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		
QY	1 MICQKFCVVLHWEFIYVITAFNLSYPITPWRFKLSMPNSTYDYFLLPAGLSKNTSNS	60
Db		
QY	61 NGHYETAPEKPNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db		
QY	121 QQIDANWNIQWLKGDGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVELEDSPLVPQKGS	180
Db		
QY	181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDPP	240
Db		
QY	241 LGLHMEITDGNLKISWSSPLVPFPPLQYQVKYSENSTTVIREADKIYKKNKI	300
Db		
QY	301 GSSYEYQVRGKRLDGPGLGSDWSTPRVFTTQDVYFPPKILTSVGSNVSPFHCYKKNKI	360
Db		
QY	361 VPSKEIYVWMMNLAEKIPQSQYDVSDHVSQVTFEENLNKTPRGKFTYDAVYCCNEHECHH	420
Db		
QY	421 RYAELYVIDVNIINISCETDGYLTWKTCRWSTSTIQSLAESTLQLRHRSLLYCSIDPSIH	480
Db		
QY	481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP	540
Db		
QY	541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV	600
Db		

Db	541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV	600
QY	601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db		
QY	661 TLLWKPLMKNDLCSVQRYVINHHTSCNGTWSEDEVGNHTKFTFLWTEQAHTVTVLAINSI	720
Db		
QY	721 GASVANFNLTSPWMSKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED	780
Db		
QY	781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSETQDDIEKHQSDA	840
Db		
QY	841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSSWAQGLNFQK	891
Db		
QY	891 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSSWAQGLNFQK	891
Db		
RESULT 10		
Q9QWG3	PRELIMINARY;	PRT; 1162 AA.
AC	Q9QWG3;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	LEPTIN RECEPTOR B.	
GN	LEPR OR LEPRB.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=KK OBESE; TISSUE=BRAIN, HYPOTHALAMUS;	
RA	Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,	
RA	Joost H.G.;	
RT	"Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,	
RT	hyperinsulinemic KK mouse strain.";	
RL	J. Endocrinol. 21:337-345(1998).	
DR	EMBL; Y10296; CAA71342.1; -.	
DR	HSSP; P16471; 1BP3.	
DR	MGI; 104993; Lepr.	
DR	InterPro; IPR002996; CRLA.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR003529; Hematopo_receptor_L_F2.	
DR	InterPro; IPR003531; Hematopo_receptor_S_F1.	
DR	Pfam; PF00041; fn3; 3.	
DR	SMART; SM00060; FN3; 3.	
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.	
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.	
KW	Receptor.	
FT	VARIANT	600 600 N -> D.
SQ	SEQUENCE	1162 AA; 130787 MW; 541e77cbb46ec00d CRC64;
Query Match 76.1%; Score 4761.5; DB 11; Length 1162;		
Best Local Similarity 75.3%; Pred. No. 0;		
Matches 878; Conservative 116; Mismatches 167; Indels 5; Gaps 5;		
QY	1 MICQKFCVVLHWEFIYVITAFNLSYPITPWRFKLSMPNSTYDYFLLPAGLSKNTSNS	60
Db		
QY	61 NGHYETAPEKPNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db		
QY	121 QQIDANWNIQWLKGDGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVELEDSPLVPQKGS	180
Db		

Db 121 RQLGVNDIECWMKGDLTFLFICHMEPLPKNPFKNYDSKVHLLYDLPEVIDDSPLPLKDS 180
Qy 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLSVQPINVMVKPDPP 240
Db 181 FQVQCNCSLRG-CECHVPVPRAKLYALLMYLEITSAGVSFQSPLSLQMLVVKPDPP 239
Qy 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 240 LGLHMEVTDGNNLKISWDSQTMAPPPLQYQVKYLENS-TIVREAAEIVSATSLLVDSVLP 298
Qy 301 GSSYEQVRGKRDLGGIWSDSWSPRVFTTQDVVYFPPKILTSVGSNVSFHCYKKNKI 360
Db 299 GSSYEQVRGKRDLGGVWSWSSPQVFTTQDVVYFPPKILTSVGSNASFHCYKKNQI 358
Qy 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 ISSKQIVWRNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEQACHH 418
Qy 421 RYAELYVIDVNNINISCETDGYLTAKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 419 RYAELYVIDVNNINISCETDGYLTAKMTCRWSPSTIQSLVGSTVQLRYHRRSLYCPDSPSIH 478
Qy 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSDSPPTCVLPDSVVKPLPP 540
Db 479 PTSEPKNCVLQRDGFYECVFQPIFLLSGYTMWIRINHSLGSDSPPTCVLPDSVVKPLPP 538
Qy 541 SSVKAEITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 539 SNVKAETVNTGLLKVSWEKVPFPENNLFQIRYGLSGKEIQWKTHEVFDKSKSASLLV 598
Qy 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 SNLCVAVYVQVRCRRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRKMDGVTKKERNV 658
Qy 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSQVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 659 TLLWKPLTKNDSLCSVRRYVVKHRTAHNGTWSQVGNHTKFTFLWTEQAHTVTVLAVNSL 718
Qy 721 GASVANFNLTFSPWMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 719 GASLVNFNLTFSWPMSKVSAVESLSAYPLSSCVILSWTLSPDDYSLLYLVIEWKILNED 778
Qy 781 GEIKWLRISSSVKKYIYIHDHFIPIEKYQFSLYPIFMQGVGKPKIINSFTQDDIEKHQSDA 840
Db 779 DGMKWLRIPSNVKKFYIHDHFIPIEKYQFSLYPVFMQGVGKPKIINGFTKDAIDKQQNDA 838
Qy 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCWQAQGLNFQKPEFHLFI 900
Db 839 GLYVIVPVISSCVLLGLTLLISHQRMKKLFWDDVPNPKNCWQAQGLNFQKPEFHLFI 898
Qy 901 KHTASVTCGPPLLEPETISEDIVDTSWKNKDEMPTTVVSLSTT-DLEKGSVCISDQF 959
Db 899 KHAESVIPGPLLEPEPISEISVDTAWKNKDEMVPAAVSLTLTPDPRESSICISDQC 958
Qy 960 NSVNFSEABGTEVTYEDESQRPQFVKYATLISNKPSETGEEQGLINSSVTKCFSSKNSP 1019
Db 959 NSANFSGSQSTQVTCEDQRPQFVKYATLVSNKLVETDEEQGFTHSPVSNICISSNHSP 1018
Qy 1020 LKDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLEGNFPEENNKKSIYY 1079
Db 1019 LRQSFSSSSWETEAOQFFLLSDQPTMISPOLSFS-GLDELLEGSFPEENHREKSVCY 1077
Qy 1080 LGVTSIKKRESGVLLTDKSRVSCPEPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFE 1139
Db 1078 LGVTSVNRRESGVLLTGEAGILCTFPAQCLFSDIRILQERCSEHFVENNLSLGTSG-ENFV 1136
Qy 1140 SYMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1137 PYMPQFQTCSTHSHKIMENKMCDLTV 1162

RESULT 11

Q9MYK9
ID Q9MYK9 PRELIMINARY; PRT; 925 AA.
AC Q9MYK9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LEPTIN RECEPTOR SHORT INSERT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys."
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF225875; AAF35389.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 925 AA; 105721 MW; EC09C27EC29C5F3A CRC64;

Query Match 73.4%; Score 4591; DB 6; Length 925;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 850; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTYDFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFICVITAFNLSYPITPWRFKLSCMPNSTYDFLLPAGLSKNTSNL 60
Qy 61 NGHJETAVEPKFNSSGTHFSNLSKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHJETAVE--FNSSDTHFSNLSKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSVF 118
Qy 121 QQIDANWNIQCWLKGDCLKFICYVESLEKFNLYNRYKVVHLLYVLPVELEDSPLVPQKGS 180
Db 119 QQMGANWNIQCWLKGDCLKFICYVESLEKFNPKNYKHVHLLYVLPVELEDSPLVPQKGS 178
Qy 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLSVQPINVMVKPDPP 240
Db 179 FQMVHCNCSVHERCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLSVQPINVMVKPDPP 238
Qy 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 239 LGLRMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDGILP 298
Qy 301 GSSYEQVRGKRDLGGIWSDSWSPRVFTTQDVVYFPPKILTSVGSNVSFHCYKKNKI 360
Db 299 GSSYEQVRGKRDLGGIWSDSWSPRVFTTQDVVYFPPKILTSVGSNVSFHCYKKNKI 358
Qy 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIYWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 418
Qy 421 RYAELYVIDVNNINISCETDGYLTAKMTCRWSTSTIQSLAESTLQRLYHRRSLYCSIDPSIIH 480


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|||||
Db 419 RYAEIYVIDVNIINISCEIDGHLTKMTCRWSTNTIQSLAGSTLQLRYSRLSSLYCFDIPSIH 478
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 479 PISKPKDCYLOSDGFYECVFPQPIFLLSGYTMWIRINHPGLSLDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVDYDAKSYSVLPV 600
Db 539 SSVKAEIKNIGLLKISWEKPVFPENNLFQIRYGLSGKEIQWKMYDVIDYDAKSYSVLPV 598
QY 601 PDLCAVYAVQVRCRRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDFCAVYAVQVRCRSDGLGLWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
QY 661 TLLWKPLMKNDLSQSVQRYVINHHHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 659 TLLWKPLMKNESLQSVQRYVINHHHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMSKVNIQVLSLSAYPLNSSCVIWSILSPSDYKLMYFIEWKNLNED 780
Db 719 GASVANFNLTFSWPMSKVNIQVLSLSAYPLNSSCVIWSILSPSDYKLMYFIEWKNLNED 778
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 779 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFAQDNTEKHQND 838
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVDPNPKNCSWAAGLNFQKPTF 895
Db 839 GLYVIVPVISSSILLGLTLLILHORMKKLFWEDVDPNPKNCSWAAGLNFQKIRGF 893

RESULT 12
Q9MYL1 PRELIMINARY; PRT; 894 AA.
AC Q9MYL1;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR SHORT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF225873; AAF35387.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 894 AA; 102191 MW; B3CAF032238BAFB9 CRC64;
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Query Match 73.4%; Score 4590; DB 6; Length 894;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 849; Conservative 15; Mismatches 25; Indels 2; Gaps 1;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCHMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCHMPPNSTYDYFLLPAGLSKNTSNL 60
QY 61 NGHETAVEPKFNSSGTHFNSLTKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVE--FNSSDTHFNSLTKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSSVF 118
QY 121 QQIDANWNIOQWLKGLKLFICYVESLTKNLFNRYNYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 119 QQMGANWNIOQWLKGLKLFICYVESLTKNPFKNYKHVHLLYVLPEVLEDSPLVPQKGS 178
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 179 FQMVHCNCSVHERCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 238
QY 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 239 LGLRMEITDDGNLKIWSSSPPLVPFPLOYEVKYSENSTTVIREADKIVSATSLLVDGILP 298
QY 301 GSSYEVQVRGKRLDGPISWSDWSTPRVFTTQDVIYPPPKILTSGSNVSFHCYKKNKI 360
Db 299 GSSYEVQVRGKRLDGPISWSDWSTPHVFTTQDVIYPPPKILTSGSNVSFHCYKKNKI 358
QY 361 VPSKEIYVWMNLAEKIPQSYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIYVWMNLAEKIPQSYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAEIYVIDVNIINISCEIDGYLTMTKTCRWSTSTIQSLAESTLQLRYSRLSSLYCSDIPSIH 480
Db 419 RYAEIYVIDVNIINISCEIDGHLTKMTCRWSTNTIQSLAGSTLQLRYSRLSSLYCSDIPSIH 478
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 479 PISKPKDCYLOSDGFYECVFPQPIFLLSGYTMWIRINHPGLSLDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVDYDAKSYSVLPV 600
Db 539 SSVKAEIKNIGLLKISWEKPVFPENNLFQIRYGLSGKEIQWKMYDVIDYDAKSYSVLPV 598
QY 601 PDLCAVYAVQVRCRRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDFCAVYAVQVRCRSDGLGLWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
QY 661 TLLWKPLMKNDLSQSVQRYVINHHHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 659 TLLWKPLMKNESLQSVQRYVINHHHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMSKVNIQVLSLSAYPLNSSCVIWSILSPSDYKLMYFIEWKNLNED 780
Db 719 GASVANFNLTFSWPMSKVNIQVLSLSAYPLNSSCVIWSILSPSDYKLMYFIEWKNLNED 778
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 779 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFAQDNTEKHQND 838
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVDPNPKNCSWAAGLNFQK 891
Db 839 GLYVIVPVISSSILLGLTLLILHORMKKLFWEDVDPNPKNCSWAAGLNFQK 889

RESULT 13
Q9MZS2
ID Q9MZS2 PRELIMINARY; PRT; 848 AA.
AC Q9MZS2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR (FRAGMENT).
```


QY	1022	DSFSNSSWEIEAQAFILSDQ---HP---NIISPHLTFSEGLDELLKLEGNFPEENNDK	1074
Dd	1011	GVCSSGSSWELGSEEFULLPDQPGSRPCKTILSLIS-----SEGSESPSQDDAFTDGGSP	1065
QY	1075	KSIYYLGVTSIKKRESGVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNIN-LGTS	1133
Dd	1066	RGLCYLGITSLDKRENAIFLTSSRLMCHFTADLLRGVGFLOQT-----PPNLNAFLQS	1120
QY	1134	SKKTFASYMPQFQTCSTQTHKIMEN	1158
Dd	1121	SIKAIVPYVPQFQMTAAKVQETTEN	1145

Search completed: August 15, 2002, 16:35:36
Job time: 796 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:24:10 ; Search time 28.14 Seconds
(without alignments)
1602.995 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEPIVIT.....QTCSTQTHKIMENKMCDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	6246	99.9	1165	1 LEPR_HUMAN	P48357 homo sapien
2	4784.5	76.5	1162	1 LEPR_RAT	Q62959 rattus norv
3	4766.5	76.2	1162	1 LEPR_MOUSE	P48356 mus musculu
4	366	5.9	917	1 IL6B_MOUSE	Q00560 mus musculu
5	345.5	5.5	918	1 IL6B_HUMAN	P40189 homo sapien
6	339.5	5.4	918	1 IL6B_RAT	P40190 rattus norv
7	313	5.0	837	1 GCSR_MOUSE	P40223 mus musculu
8	294.5	4.7	1097	1 LIFR_HUMAN	P42702 homo sapien
9	284	4.5	836	1 GCSR_HUMAN	Q99062 homo sapien
10	281.5	4.5	1092	1 LIFR_MOUSE	P42703 mus musculu
11	220.5	3.5	862	1 IL2S_HUMAN	Q99665 homo sapien
12	220	3.5	830	1 PRLR_COLLI	Q90374 columba liv
13	220	3.5	874	1 IL2S_MOUSE	P97378 mus musculu
14	209.5	3.3	831	1 PRLR_CHICK	Q04594 gallus gall
15	190	3.0	831	1 PRLR_MELGA	Q91094 meleagris g
16	184	2.9	2481	1 FIRC_XENLA	Q91740 xenopus lae
17	173.5	2.8	1493	1 NEOL_MOUSE	P97798 mus musculu
18	172	2.8	2012	1 DSCA_HUMAN	O60469 homo sapien
19	170.5	2.7	1461	1 NEOL_HUMAN	Q92859 homo sapien
20	169.5	2.7	1443	1 NEOL_CHICK	Q90610 gallus gall
21	166.5	2.7	2029	1 LAR_DROME	P16621 drosophila
22	165	2.6	630	1 PRLR_ORENI	Q91513 oreochromis
23	162	2.6	1447	1 DCC_MOUSE	P70211 mus musculu
24	158.5	2.5	462	1 IL6A_RAT	P22273 rattus norv
25	154.5	2.5	2386	1 FIRC_HUMAN	P02751 homo sapien
26	153.5	2.5	460	1 IL6A_MOUSE	P22272 mus musculu
27	151	2.4	1377	1 NEOL_RAT	P97603 rattus norv
28	150.5	2.4	610	1 PRLR_RAT	P05710 rattus norv
29	147.5	2.4	638	1 GHR_MACMU	P79194 macaca mula
30	146	2.3	3063	1 CALC_HUMAN	Q99715 homo sapien
31	145.5	2.3	2477	1 FIRC_RAT	P04937 rattus norv
32	144.5	2.3	1302	1 NRG_DROME	P20241 drosophila
33	144	2.3	581	1 PRLR_CEREL	Q28235 cervus elap

RESULT 1					
LEPR_HUMAN					
ID	LEPR_HUMAN	STANDARD;	PRT;	1165	AA.
AC	P48357;				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).				
GN	LEPR OR OBR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=96128129; PubMed=8548812;				
RA	Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,				
RA	Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,				
RA	Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,				
RA	Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;				
RT	"Identification and expression cloning of a leptin receptor, OB-R.";				
RL	Cell 83:1263-1271(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Thompson D.B., Ossowski V., Sutherland J., Apel W.,				
RA	Bierstfeldt J.;				
RL	Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.				
RN	[3]				
RP	VARIANT ARG-223.				
RX	MEDLINE=96270489; PubMed=8666155;				
RA	Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;				
RT	"The hypothalamic leptin receptor in humans: identification of				
RT	incidental sequence polymorphisms and absence of the db/db mouse and				
RT	fa/fa rat mutations.";				
RL	Diabetes 45:992-994(1996).				
RN	[4]				
RP	VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.				
RX	MEDLINE=97289527; PubMed=9144432;				
RA	Echwald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,				
RA	Andersen T., Chung W.K., Leibel R.L., Pedersen O.;				
RT	"Amino acid variants in the human leptin receptor: lack of association				
RT	to juvenile onset obesity.";				
RL	Biochem. Biophys. Res. Commun. 233:248-252(1997).				
RN	[5]				
RP	VARIANTS ARG-109; ARG-223 AND ASN-656.				
RX	MEDLINE=97431549; PubMed=9287054;				
RA	Chung W.K., Power-Kehoe L., Chua F., Aronne L., Huma Z.,				
RA	Sothorn M., Udall J.N., Kahle B., Leibel R.L.;				
RT	"Exonic and intronic sequence variation in the human leptin receptor				
RT	gene (LEPR).";				
RL	Diabetes 46:1509-1511(1997).				
RN	[6]				
RP	VARIANTS ARG-109 AND ARG-223.				
RX	MEDLINE=97301763; PubMed=9158141;				
RA	Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;				

34	143.5	2.3	1447	1	DCC_HUMAN	P43146 homo sapien
35	143	2.3	638	1	GHR_HUMAN	P10912 homo sapien
36	142.5	2.3	3135	1	S230_PLAFO	Q08372 plasmodium
37	141	2.3	581	1	PRLR_BOVIN	Q28172 bos taurus
38	141	2.3	878	1	IL3B_MOUSE	P26954 mus musculu
39	140.5	2.2	638	1	GHR_PIG	P19756 sus scrofa
40	140.5	2.2	638	1	GHR_RABIT	P19941 oryctolagus
41	139	2.2	635	1	TPOR_HUMAN	P40238 homo sapien
42	138	2.2	1897	1	PTPF_HUMAN	P10586 homo sapien
43	138	2.2	2265	1	FIRC_BOVIN	P07589 bos taurus
44	136	2.2	928	1	PMP9_CHLPN	Q92398 chlamydia p
45	135.5	2.2	1013	1	EPA5_CHICK	P54755 gallus gall

ALIGNMENTS

RT *Structure and sequence variation at the human leptin receptor gene in
RT lean and obese Pima Indians.";
RL Hum. Mol. Genet. 6:675-679(1997).
RN [7]
RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
RX MEDLINE=99075638; PubMed=9860295;
RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,
RA Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
RT "Transmission disequilibrium and sequence variants at the leptin
RT receptor gene in extremely obese German children and adolescents.";
RL Hum. Genet. 103:540-546(1998).
RN [8]
RP VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE=97318795; PubMed=9175732;
RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,
RA Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;
RT "Leptin receptor gene variation and obesity: lack of association in a
RT white British male population.";
RL Hum. Mol. Genet. 6:869-876(1997).
CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; U43168; AAA93015.1; -.
DR EMBL; U59263; AAB09673.1; -.
DR EMBL; U59248; AAB09673.1; JOINED.
DR EMBL; U59249; AAB09673.1; JOINED.
DR EMBL; U59250; AAB09673.1; JOINED.
DR EMBL; U59252; AAB09673.1; JOINED.
DR EMBL; U59253; AAB09673.1; JOINED.
DR EMBL; U59254; AAB09673.1; JOINED.
DR EMBL; U59255; AAB09673.1; JOINED.
DR EMBL; U59256; AAB09673.1; JOINED.
DR EMBL; U59257; AAB09673.1; JOINED.
DR EMBL; U59258; AAB09673.1; JOINED.
DR EMBL; U59259; AAB09673.1; JOINED.
DR EMBL; U59260; AAB09673.1; JOINED.
DR EMBL; U59261; AAB09673.1; JOINED.
DR EMBL; U59262; AAB09673.1; JOINED.
DR HSSP; P40189; 1BQU.
DR MIM; 601007; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Polymorphism.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 1165 LEPTIN RECEPTOR.
FT DOMAIN 22 841 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 842 862 POTENTIAL.
FT DOMAIN 863 1165 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 237 320 FIBRONECTIN TYPE-III 1.
FT DOMAIN 537 623 FIBRONECTIN TYPE-III 2.
FT DOMAIN 738 823 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	276	276	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	347	347	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	433	433	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	516	516	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	659	659	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	688	688	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	697	697	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	728	728	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	VARIANT	109	109	K -> R.	
FT	VARIANT	204	204	/FTid=VAR_002703.	
FT	VARIANT	223	223	K -> R.	
FT	VARIANT	656	656	/FTid=VAR_002704.	
FT	VARIANT	675	675	Q -> R.	
FT	VARIANT	675	675	/FTid=VAR_002705.	
FT	VARIANT	675	675	K -> N.	
FT	VARIANT	675	675	/FTid=VAR_002706.	
FT	VARIANT	675	675	S -> T.	
FT	VARIANT	675	675	/FTid=VAR_002707.	
SQ	SEQUENCE	1165	AA; 132449	MW; 8FF21D9AF5125808	CRC64;

Query Match 99.9%; Score 6246; DB 1; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MICQKFCVLLHWEFYVITAFNL	SYPTTPWRKLS	CMPPNSTYDYFLLPAGLSKNTS	NS 60	
Db	1	MICQKFCVLLHWEFYVITAFNL	SYPTTPWRKLS	CMPPNSTYDYFLLPAGLSKNTS	NS 60	
QY	61	NGHYETAVEPKFNSSGTHFSNLS	KTTFHCCFRSQDRNC	SLCADNIEGKTFVTVNSLVF	120	
Db	61	NGHYETAVEPKFNSSGTHFSNLS	KTTFHCCFRSQDRNC	SLCADNIEGKTFVTVNSLVF	120	
QY	121	QQIDANWNIQWLKGLKLFICYVES	LKFNFRNYKVHLLYL	VLPVLEDSPLVPQKGS	180	
Db	121	QQIDANWNIQWLKGLKLFICYVES	LKFNFRNYKVHLLYL	VLPVLEDSPLVPQKGS	180	
QY	181	FQMVHCNCSVHECCCLVPVPTAK	LNDTLLMCLKITSGG	VIFQSPLMSVQPINMVKPDPP	240	
Db	181	FQMVHCNCSVHECCCLVPVPTAK	LNDTLLMCLKITSGG	VIFQSPLMSVQPINMVKPDPP	240	
QY	241	LGLHMEITDDGNLKSWSPPPLVP	FPFLOQYQVYSENST	TVIREADKIVSATSLLVDSILP	300	
Db	241	LGLHMEITDDGNLKSWSPPPLVP	FPFLOQYQVYSENST	TVIREADKIVSATSLLVDSILP	300	
QY	301	GSSYEYQVRGKRLDGP	GIWSDWSTPRVFTTQDVIYFP	PKILTSVGSNVSFHCYKKNKI	360	
Db	301	GSSYEYQVRGKRLDGP	GIWSDWSTPRVFTTQDVIYFP	PKILTSVGSNVSFHCYKKNKI	360	
QY	361	VPSKEIVWMNLAEKIPQSQYDV	SDVSDHVS	SKVTFFNLNETKPRGKFTYDAYCCNEHECHH	420	
Db	361	VPSKEIVWMNLAEKIPQSQYDV	SDVSDHVS	SKVTFFNLNETKPRGKFTYDAYCCNEHECHH	420	
QY	421	RYAELYVIDVNI	INISCE	TGDLTKMTCRWSTSTIQSLAESTLQLR	YHRSSLYCSDIPS	480
Db	421	RYAELYVIDVNI	INISCE	TGDLTKMTCRWSTSTIQSLAESTLQLR	YHRSSLYCSDIPS	480
QY	481	PISEPKCYLQSDGFE	YECIFQPIFLLSGYTMWIRIN	HSLSGLDSPPTCVLPD	SVVKPLPP	540
Db	481	PISEPKCYLQSDGFE	YECIFQPIFLLSGYTMWIRIN	HSLSGLDSPPTCVLPD	SVVKPLPP	540
QY	541	SSVKAETINIGL	KISWEKPVFPENN	LQFIQRYGLSGKEVQWKMYE	VDIAKSKSVSLPV	600
Db	541	SSVKAETINIGL	KISWEKPVFPENN	LQFIQRYGLSGKEVQWKMYE	VDIAKSKSVSLPV	600
QY	601	PDLCAVYAVQVRCK	RLDGLGYWSNWSNPAYTV	VMDIKVPMRGPEFWRI	INGDTMKKEKNV	660
Db	601	PDLCAVYAVQVRCK	RLDGLGYWSNWSNPAYTV	VMDIKVPMRGPEFWRI	INGDTMKKEKNV	660

QY 661 TLLWKPLMKNDLSCSVQRYVINHHHTSCNGTWSEVGNHKTFTFLWTEQAHTVTVLAINSI 720
D6 661 TLLWKPLMKNDLSCSVQRYVINHHHTSCNGTWSEVGNHKTFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSSCVIYVSWILSPSDYKLMYFIIENKLNLED 780
D6 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSSCVIYVSWILSPSDYKLMYFIIENKLNLED 780
QY 781 GEIKWLRISSSVKKYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIERHQSDA 840
D6 781 GEIKWLRISSSVKKYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIERHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLFWEVDPNPKNCSSWAQGLNFQKPFTEHLFI 900
D6 841 GLYVIVPVISSSILLGLTLLISHQRMKLFWEVDPNPKNCSSWAQGLNFQKPFTEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDIVSDTSWKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960
D6 901 KHTASVTCGPLLEPETISEDIVSDTSWKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEAGTEVTEYDESRQPFVKYATLISNSKPSFTEGEEQGLNLSVTKCFSSKNSPL 1020
D6 961 SVNFSEAGTEVTEYAEQRQPFVKYATLISNSKPSFTEGEEQGLNLSVTKCFSSKNSPL 1020
QY 1021 KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYYL 1080
D6 1021 KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFFAS 1140
D6 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMCIDLTV 1165
D6 1141 YMPQFQTCSTQTHKIMENKMCIDLTV 1165
RESULT 2
LEPR_RAT STANDARD; PRT; 1162 AA.
AC Q62959; Q63007; P70493; P70494; P70495; Q63385; Q63386; Q54805;
AC P97589; Q35772;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEP-R OR OBR OR FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN-ZUCKER; TISSUE-Hypothalamus;
RX MEDLINE-96241565; PubMed-8673096;
RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
RA Hess J.F.;
RT "Leptin receptor missense mutation in the fatty Zucker rat.";
RL Nat. Genet. 13:18-19(1996).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE-Brain;
RX MEDLINE-96295531; PubMed-8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Substitution at codon 269 (glutamine --> proline) of the leptin
RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
RT (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANTS A; B AND E).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE-96332408; PubMed-8769097;

RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,
RA Mori K., Tamura N., Hosoda K., Nakao K.;
RT "Molecular cloning of rat leptin receptor isoform complementary
RT DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)
RT rats.";
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT B).
RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
RA Carlsson B.;
RT "Cloning of the rat leptin receptor.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE-96212906; PubMed-8630068;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
RT Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
RN [6]
RP SEQUENCE OF 1-123 FROM N.A.
RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;
RT "Analysis of rat leptin receptor gene.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 694-878 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;
RA Ma Z.;
RT "Identification of a leptin receptor in islet.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
RC STRAIN-SPRAGUE-DAWLEY;
RA Chien E.K., Hara M., Rouard M., Yano H., Phillippe M., Polonsky K.S.,
RA Bell G.I.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [9]
RP VARIANT FA PRO-269.
RX MEDLINE-96314329; PubMed-8690163;
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
RA Leibel R.L.;
RT "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
RT (Lepr).";
RL Diabetes 45:1141-1143(1996).
CC -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
CC -!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
CC WHICH COULD BE SECRETED.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHIVERING
CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
CC TISSUE.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U52966; AAC52587.1; -.
DR EMBL; D84550; BAA12697.1; -.
DR EMBL; D84551; BAA12698.1; -.
DR EMBL; D85557; BAA12830.1; -.

DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219
DE receptor).
GN LEPR OR OBR OR DB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT A).
RC TISSUE=Choroid plexus;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Mulr C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;
RT "Identification and expression cloning of a leptin receptor, OB-R.";
RL Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;
RX MEDLINE=96190816; PubMed=8608603;
RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
RA Duyk G.M., Tepper R.I., Morgenstern J.P.;
RT "Evidence that the diabetes gene encodes the leptin receptor:
RT identification of a mutation in the leptin receptor gene in db/db
RL mice.";
RL Cell 84:491-495(1996).
RN [3]
RP SEQUENCE FROM N.A. (VARIANTS A TO E).
RC STRAIN=C57BL/KS; TISSUE=Hypothalamus;
RX MEDLINE=96231997; PubMed=8628397;
RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
RA Lee J.I., Friedman J.M.;
RT "Abnormal splicing of the leptin receptor in diabetic mice.";
RL Nature 379:632-635(1996).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT C).
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
RA Mikhail A., Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
RN [5]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN=NEW ZEALAND OBESE / NZO; TISSUE=Hypothalamus;
RX MEDLINE=97462708; PubMed=9322935;
RA Igel M., Becker W., Herberg L., Joost H.G.;
RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor
RT in the New Zealand obese mouse.";
RL Endocrinology 138:4234-4239(1997).
RN [6]
RP SEQUENCE FROM N.A. (VARIANTS A AND B).
RC STRAIN=FVB/N; TISSUE=Spleen;
RX MEDLINE=96270520; PubMed=8692797;
RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,
RA Skoda R.C.;
RT "Defective STAT signaling by the leptin receptor in diabetic mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
RN [7]
RP SEQUENCE FROM N.A. (VARIANT E).
RC STRAIN=129/J;
RX MEDLINE=98008913; PubMed=9344648;
RA Chua S.C., Koutiras I.K., Han L., Liu S.M., Kay J., Young S.J.,
RA Chung W.K., Leibel R.L.;
RT "Fine structure of the murine leptin receptor gene: splice site
RT suppression is required to form two alternatively spliced
RL transcripts.";
RL Genomics 45:264-270(1997).
CC -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CC -!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
CC WHICH COULD BE SECRETED.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN
CC LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.
CC (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND
CC LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E:
CC EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL; U42467; AA93014.1; -
DR EMBL; U46135; AAC52408.1; -
DR EMBL; U49106; AAC52420.1; -
DR EMBL; U49107; AAC52421.1; -
DR EMBL; U49108; AAC52422.1; -
DR EMBL; U49109; AAC52423.1; -
DR EMBL; U49110; AAC52424.1; -
DR EMBL; U52915; AAC52599.1; -
DR EMBL; Y10298; CAA71343.1; -
DR EMBL; U58861; AAC52705.1; -
DR EMBL; U58862; AAC52706.1; -
DR EMBL; U58863; AAC52707.1; -
DR EMBL; AF039456; AAB95334.1; -
DR EMBL; AF039443; AAB95334.1; JOINED.
DR EMBL; AF039444; AAB95334.1; JOINED.
DR EMBL; AF039445; AAB95334.1; JOINED.
DR EMBL; AF039446; AAB95334.1; JOINED.
DR EMBL; AF039447; AAB95334.1; JOINED.
DR EMBL; AF039448; AAB95334.1; JOINED.
DR EMBL; AF039449; AAB95334.1; JOINED.
DR EMBL; AF039450; AAB95334.1; JOINED.
DR EMBL; AF039451; AAB95334.1; JOINED.
DR EMBL; AF039452; AAB95334.1; JOINED.
DR EMBL; AF039453; AAB95334.1; JOINED.
DR EMBL; AF039454; AAB95334.1; JOINED.
DR EMBL; AF039455; AAB95334.1; JOINED.
DR HSSP; P40189; 1BQU.
DR MGD; MGI:104993; Lepr.
DR InterPro; IPR002996; CRLA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Polymorphism; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 1162 LEPTIN RECEPTOR.
FT DOMAIN 22 839 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 840 860 POTENTIAL.
FT DOMAIN 861 1162 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 318 FIBRONECTIN TYPE-III 1.
FT DOMAIN 535 621 FIBRONECTIN TYPE-III 2.
FT DOMAIN 736 821 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 41 41 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).

FT	CARBOHYD	345	345	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	431	431	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	514	514	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	622	622	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	657	657	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	668	668	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	686	686	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	695	695	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	698	698	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	726	726	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	VARSPLIC	890	894	PETFE -> RTDTL (IN ISOFORM A).	
FT	VARSPLIC	895	1162	MISSING (IN ISOFORM A).	
FT	VARSPLIC	890	892	PET -> VTV (IN ISOFORM C).	
FT	VARSPLIC	893	1162	MISSING (IN ISOFORM C).	
FT	VARSPLIC	890	900	PETFEHLFTKH -> DISFHEVFIER (IN ISOFORM D).	
FT	VARSPLIC	901	1162	MISSING (IN THE ISOFORM D).	
FT	VARSPLIC	797	805	DNFPIEKY -> GMCTVLFMD (IN ISOFORM E).	
FT	VARSPLIC	806	1162	MISSING (IN ISOFORM E).	
FT	VARIANT	541	541	V -> I (IN STRAIN NOZ).	
FT	VARIANT	651	651	V -> I (IN STRAIN NOZ).	
FT	VARIANT	1044	1044	T -> I (IN STRAIN NOZ).	
FT	CONFLICT	140	140	F -> I (IN REF. 6).	
FT	CONFLICT	720	720	A -> T (IN REF. 5).	
SQ	SEQUENCE	1162 AA;	130788 MW;	0E1E75B076BA60A2 CRC64;	
Query Match 76.2%; Score 4766.5; DB 1; Length 1162;					
Best Local Similarity 75.4%; Pred. No. 0;					
Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;					
Qy	1	MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCLMPNPNSTYDYFLLPAGLSKNTSNS	50		
Db	1	MMQKFFYVLLHWEFLYVIAALNLAYIPSPWKFKLFCGPPNTTDDSLSPAGAPNNASAL	50		
Qy	61	NGHYETAVEKFNSSGTHFNSLSKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVP	120		
Db	61	KGASEAIVEAKFNSSGIYVPELSKTVFHCFCGNEQGQNCALSALTDNTEGKTLASVVKASVF	120		
Qy	121	QQIDANNIQCWLKGDCLKFICYVESLFKNLFRNRYNKKVHLLYVLPDEVLEDSPLVPQKGS	180		
Db	121	RLQGVNWDIECWKMGDLTLFICHMEPLPKNPFKNYDSKVHLLYDLPEVIDDSPLPLKDS	180		
Qy	181	FQVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGVIFQSPLMSVQPINVMVKPDPP	240		
Db	181	FQTVQCNCSLRG-CECHVPVPRAKLNALLMYLEITSAGVSFQSPLMSLQPMVLVVKPDPP	239		
Qy	241	LGLHMEITDDGNLKISWSSPPLVPFPFLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP	300		
Db	240	LGLHMEVTDGDNLKISWDSQTMAPPFLOQYQVYKYLENS-TIVREAAEIVSATSLLVDSVLP	298		
Qy	301	GSSYEVOVGRKRLDGPICISWDSWSTPRVFTQDVIYFPFKILTSVGSNSVFHFCIYKKENKI	360		
Db	299	GSSYEVOVRSKRLDGSVWSDSSPQVFTQDVVYFPFKILTSVGSNASFHCYKKNENQI	358		
Qy	361	VPSKEIYVWMNLAEKIPQSOYDVVSDHVSQVTFNLTNETKPRGFTYDAVYCCNEHECHH	420		
Db	359	ISSKQIYVWRNLAEKIPETQSIYSDRVSKVTFNSNLKATRPGRGFTYDAVYCCNEQACHH	418		
Qy	421	RYAELYVIDVINISCETDGYLTQMTCRWSTSTIQSLAESTLQLYRHRSSLYCSDIPSIIH	480		
Db	419	RYAELYVIDVINISCETDGYLTQMTCRWSPSTIQSLVGSTVQLRYHRRSLYCPDPSIIH	478		
Qy	481	PISEPKCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	540		
Db	479	PTSEPKNCVLQDGFYECVCFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	538		
Qy	541	SSVKAETITNGLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV	600		
Db	539	SNVKAETITNGLKISWEKPVFPENNLFQIRYGLSGKEIQWKTHEVFDKSKSASLLV	598		
Qy	601	PDLCAYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWIRINGDTMKKEKNV	660		

Db	599	SDLCAYVVQVRCRRLDGLGYWSNWSNPAYTLVMDVKVPMRGPEFWRKMDGDVTKKERNV	658		
Qy	661	TLLWKPLMKNDLSCSVQRYVINHHTSCNGTWSESDVGNHTKFTFLWTEQAHTVTVLAINSI	720		
Db	659	TLLWKPLTKNDLSCSVRRYVVKHRTAHNGTWSESDVGNRTNLTLWTEPAHTVTVLAVNSL	718		
Qy	721	GASVANENLTFSPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED	780		
Db	719	GASLVNENLTFSPMSKVSAYESLSSCVILSWTLSPDDYSLLYLVIEWKILNED	778		
Qy	781	GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA	840		
Db	779	DGMKWLRIIPSNVKKFYIHDNEFIPIEKYQFSLYPVFMGVGKPKIINGFTKDAIDKQONDA	838		
Qy	841	GLYVIVPVISSILLGLTLISHQRMKKLFWEDVPNPKNCSSWAGLNFQKPFTEHLEFI	900		
Db	839	GLYVIVPIIISSCVLLGLTLISHQRMKKLFWDDVPNPKNCSSWAGLNFQKPFTEHLEFI	898		
Qy	901	KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTT-DLEKGSVCISDQF	959		
Db	899	KHAESVIFGPLLLEPEPISEISVDTAKNKDEMVPAAVMSLLLTTPDPSESSICISDQC	958		
Qy	960	NSVNFSEABGTEVTYEDESQRQPFVYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSP	1019		
Db	959	NSANFSGSQSTQVTCEDQCQRPQSVKYATLVSNDKLVETDEEQGFHSPVSNICISSNHSP	1018		
Qy	1020	LKDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSGLDELLKLEGNFPEENNKKSIYY	1079		
Db	1019	LRQSFSSSWETEATQTFLLSDQOQPTMISPLQSFSG-GLDELLELEGSFPEENHREKSVCY	1077		
Qy	1080	LGVTISIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFA	1139		
Db	1078	LGVTSVNRRESGVLLTGEAGILCTEPAQCLFSDIRILQERCSSHFEVNNLSLGTSG-ENFV	1136		
Qy	1140	SYMPOFQTCSTQTHKIMENKMCMLTV	1165		
Db	1137	PYMPQFQTCSTHSHKIMENKMCMLTV	1162		
RESULT 4					
IL6B_MOUSE					
ID	IL6B_MOUSE	STANDARD;	PRT;	917 AA.	
AC	Q00560;				
DT	01-FEB-1995 (rel. 31, Created)				
DT	01-FEB-1995 (rel. 31, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin 6 signal transducer) (Membrane glycoprotein 130) (GPI30).				
GN	IL6ST.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-ICR; TISSUE=Macrophage;				
RX	MEDLINE=92291532; PubMed=1602143;				
RA	Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.;				
RT	"Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130, and its regulated expression in vivo."				
RL	J. Immunol. 148:4066-4071(1992).				
CC	-!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GPI30 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.				
CC	-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE CELLS.				

RA Hibb M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RL gp130.";
RN Cell 63:1149-1157(1990).
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC MEDLINE=20341529; PubMed=10880057;
RX Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RA Murakami M., Nakao K.;
RT "Cloning of novel soluble gp130 and detection of its neutralizing
autoantibodies in rheumatoid arthritis.";
RL J. Clin. Invest. 106:137-144(2000).
RN [3]
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=21269388; PubMed=11098061;
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
RT "Determination of the disulfide structure and N-glycosylation sites of
the extracellular domain of the human signal transducer gp130.";
RL J. Biol. Chem. 276:8244-8253(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX MEDLINE=98169383; PubMed=9501088;
RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130.";
RL EMBO J. 17:1665-1674(1998).
CC -!- FUNCTION: Signal-transducing molecule. The receptor systems for
IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for
initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)
complex, resulting in the formation of high-affinity IL-6 binding
sites, and transduces the signal. Does not bind IL-6. May have a
role in embryonic development (By similarity).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and
secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/gp130-
RAPS; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Found in all the tissues and cell lines
examined. Expression not restricted to IL-6 responsive cells.
CC -!- DISEASE: gp130-RAPS is an autoantigen found in rheumatoid
arthritis (RA) but it is not specific to patients with RA.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57230; AAA59155.1; -.
DR EMBL; AB015706; BAA78112.1; -.
DR PIR; A36337; A36337.
DR PDB; 1BQU; 26-AUG-98.
DR MIM; 600694; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FN_III_repeat.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat; 3D-structure; Alternative splicing.
FT SIGNAL 1 22 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT CHAIN 23 918 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 23 619

FT	TRANSMEM	620	641	POTENTIAL.
FT	DOMAIN	642	918	CVTOPLASMIC (POTENTIAL).
FT	DOMAIN	26	120	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	124	222	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	223	324	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	325	423	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	424	517	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	518	613	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	725	755	SER-RICH.
FT	DISULFID	28	54	
FT	DISULFID	48	103	
FT	DISULFID	134	144	
FT	DISULFID	172	182	
FT	DISULFID	458	466	
FT	CARBOHYD	43	43	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	83	83	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	131	131	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	227	227	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	379	379	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	383	383	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	553	553	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	564	564	N-LINKED (GLCNAC. . .).
FT	VARSPLIC	325	329	RPSKA -> NIASF (IN GP130-RAPS).
FT	VARSPLIC	330	918	MISSING (IN GP130-RAPS).
SQ	SEQUENCE	918 AA;	103522 MW;	D813F3672DD10D53 CRC64;

Query Match 5.5%; Score 345.5; DB 1; Length 918;
Best Local Similarity 19.8%; Pred. No. 1.4e-15;
Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;

QY	337	PPKILTSVGSNVSFHCIYKK--ENKIVPSKEIVWMNLAEKIPQSQVDVSDHVSQVTF	393
DB	33	PESPVVQLHSNFTAVCVLKEKCMDFHVNANYIVWKTN-HETIPKEQVYTIINRTASSVTF	91
QY	394	FNLNETKPRGKFTYDAVCCNEHECHRYAEVLYVDV-----NINISC-ETDGYLTK	444
DB	92	TDI-----ASLNQLTCNLTFTGQLEQNVYGITISGLPPEKPKNLSCIVNEG--KK	141
QY	445	MTCRWSTSTIQSLAESTLQRYHRSSLYCSDIPSISHPISPKDCYQLQSDGFYECI--FQP	502
DB	142	MRCEWDGG-----RETHLETNFTLKSEWAT-----HKFA--DCKAKRDTPTCTVDYST	188
QY	503	IFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVVKPLPPSSVKAETIN----IGLLKISW	558
DB	189	VYFVN-IEVWVEAENALGKVTSDHINFDPYKVKPNPPHNLNLS--VINSEELSSILKLTW	244
QY	559	EKP-----VFPENNLFQFIRYGLSGKEVQMKMYEVDASKSVSLPVPDL--CAVYAVQV	611
DB	245	TNPSIKSVIILKYNIQYRTKDAST-----WSQIPPEDTASTRSSTFTVQDLKPFTEYVFR	299
QY	612	RCKRLDGLGYMNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKND	671
DB	300	RCMKEDGKGYSWSDWSEEASGITYEDR-PSKAPSFYWKIDPSHTQGYRTVQLVWKTLPPE	358
QY	672	SLCSVQRYVINHHTSCNGTWSQVGNH---TKFTFLWTEQAHTVTVLAINSIGASVANF	727
DB	359	ANGKILDYEVT-----LTRWKSHLQNYTVNATKLTNLTNDRYLATLTVRNLVGSDDAAV	413
QY	728	NLTFSPMKSVMNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIWKNNLNEDGE--IKW	785
DB	414	LTIPACDFQATHPVMDLKAFF-KDNMLWVETWTPRESVK--KYILEWCVLSDKAPCITDW	470
QY	786	LRISSSVKYYIHDHFIPIEKYQFSLYPFMGEVGVKPKII-----	825
DB	471	QQEDGTVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTVTRTKV	530
QY	826	-----	
DB	531	GKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTTEYLSLTSOT-LYM	589
QY	844	-----VIVPVISSSI-LLLGLTLLISHQR--MKK	869

Db 590 VRMAAYTDEGGKDGPEFTFTTPKFAQGEIEAIVPVCLAFLLTLLGVLCFNKRDLIKK 649
QY 870 LFWEVDVNPKNCSWAQGLNFQKPFTEHLFIKHTASVTCGPLLEPETISEDISVDTSWK 929
Db 650 HIWPNVDPSPKSHIAQWSPHTPP-----RH-----NEN 677
QY 930 NKDEMPTTVVSLSTTDLEKGSVCISDQNSVNFSEAGTEGVTYEDESQRQPF---VKY 986
Db 678 SKDQM-----YSDGNFTDVSVEIEAND---KKPFPEDLKS 710
QY 987 ATLISNKPSETGEEQGLINSSVTKCFSSKNKSPDKDSFNSS 1028
Db 711 LDLPKKEKINTEGHSSGIGGSS---CMSSSRPSISSSDENES 749

RESULT 6
IL6B_RAT ID IL6B_RAT STANDARD; PRT; 918 AA.
AC P40190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
6 signal transducer) (Membrane glycoprotein 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
transducing molecule, gp130.";
RL Genomics 14:666-672(1992).

CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC -----
CC EMBL; M92340; -; NOT_ANNOTATED_CDS.
DR PIR; A44257; A44257.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.

FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 619 640 POTENTIAL.
FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 221 FIBRONECTIN TYPE-III 1.
FT DOMAIN 222 323 FIBRONECTIN TYPE-III 2.
FT DOMAIN 324 422 FIBRONECTIN TYPE-III 3.
FT DOMAIN 423 516 FIBRONECTIN TYPE-III 4.
FT DOMAIN 517 612 FIBRONECTIN TYPE-III 5.
FT DOMAIN 724 754 SER-RICH.
FT DISULFID 28 54 BY SIMILARITY.
FT DISULFID 48 103 BY SIMILARITY.
FT DISULFID 134 144 BY SIMILARITY.
FT DISULFID 172 181 BY SIMILARITY.
FT DISULFID 457 465 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FECEFF087F7 CRC64;

Query Match 5.4%; Score 339.5; DB 1; Length 918;
Best Local Similarity 20.8%; Pred. No. 3.7e-15;
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;

QY 327 VFTTQDVI-----YFPKILTSVGSNVSFHCYKKNKIVPSKE--IVWMNLAEE 374
Db 14 IFLTTEISIGQLVEPCGYIYPEFPVQVQSGNFTATCVLKEKCLQVSVNATYIVWKTNHV- 72
QY 375 KIPQSQYDVVSDHVSKVTFNLTNETKPRKFTYDAVY-----CCNEHECHRYAELVI- 428
Db 73 AVPKQVTVINRTASSVTF-----TDVVFQNVQLTCNLSFGQIEQNVYGIT 119
QY 429 -----DVNINISC-ETDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480
Db 120 ILSGYPPDIPTNLSCIIVNEG--KNMLCQ-----LDPGRETYLETNTYTLKSEWATE----- 167
QY 481 PISEPKDCYLQSDGFYECI--FQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPL 538
Db 168 ---KFPDCRTK-HGTSSCMMGYTPIYFVN-IEVWVEAENALGNVSSEPIINFDPVDKVKPS 222
QY 539 PPSSVKAETINI-GLLKISW-----EKVPFPENNLFQIRYGLSGKEVQMKMYEVDK 592
Db 223 PPHNLSVTNSEEELSSILKAWNSGLDSILRLKSDIQYRTKDAST-----WIQVPLEDTV 277
QY 593 SKSVSLPVPDL--CAVYAVQVRCKRLDGLGYSNWSNPNPAYTVVMDIKVPMRGPEFWRIIN 650
Db 278 SPRTSFTVODLKPFTTEYVFRIRSIKENGKGYWSDWSEASGTTYEDR-PSKAPSFYKVN 336
QY 651 GDTMKKEKNVTLLWKPLMKNDLSLCSVQRY--VINHHTSCNGTWSEDEVGNHTKFTFLWTEQ 708
Db 337 ANHPQEYRSARLIWKTLPLSEANGKILDYEVVLTQSKSVSQTYTV---NGTELVNLTNN 393
QY 709 AHTVTVLAINSIGASVANFNLTFSWPMSKV-NIVQSLASAYPLNSSCVIVSWILSPDYKL 767
Db 394 RYVASLAARNVVGKSPATV-LTIPGSHFRASHPVVDLKAFF-KDNLWVEW--TPPSKPV 449
QY 768 MYFIIIEWKLNLEDGEI--KWLRISSSVKYYIYHDHFIPIEKYQFSLYPIFMGVGKPV--- 822
Db 450 NKYILEWCVLSENPCIPDWQQEDGTVNRTHLRGLSLESKCYLITVTPVPPGGPGSPESM 509
QY 823 -----KI 824
Db 510 KAYLKQAAPSKGPTVTRTKKVGKNEAVLENDHLPVDVQNGFIRNYSISYRTSVGKEMVVRV 569


```
QY 825 INSFTQDDIEKHQSDAGLY-----VIVPVISS 852
:| | : | | | | :| | | :| | | :
Db 570 DSSHTEYTLSSLSDT-LYMVHMAAYTEEGKDGPRFTFTTLKFAQGEIEAIVVPVCLAF 628
:| | | :| | | :| | | :| | | :| | | :
QY 853 SI-LLGLTLLISHQR--MKKLFWEDVPNPKNCSWAAGLNFQKPTFHLF-----IKHTA 904
:| | | :| | | :| | | :| | | :| | | :
Db 629 LLTLLGVLCFNKRDLLKHHIWPVDPSPKSHIAQWSPHTPP---RHNFNKSDQMYSDA 685
:| | | :| | | :| | | :| | | :| | | :
QY 905 SVTCGPLLLEPETISEDIVSDTSWNKDKDEMPPTVVSLSTTDLEK----- 950
:| | | :| | | :| | | :| | | :| | | :
Db 686 NPT-----DVSVVEIEANKKPCDDLKSL---DLFKKKEKISTEGHSSGIG 728
:| | | :| | | :| | | :| | | :| | | :
QY 951 GSVCIISQDNFNVFSEABEGTEVYDEESQRQ--PFVKYATLISNKPSETGEEQGLINSS 1008
:| | | :| | | :| | | :| | | :| | | :
Db 729 GSSCMSRRPSISSE-----ENESAQSTASTVQYSTVHSGYRHQVPSVQVFSRSE 780
:| | | :| | | :| | | :| | | :| | | :
QY 1009 VTK-CFSSKNSP---LKDSFSNSSWEIEAQAFFILSDQHPNIIISPHLT 1052
:| | | :| | | :| | | :| | | :| | | :
Db 781 STQPLLDSEERPEDQLVDSVDSGDEILPRQQYFKQSCSQPG-ASPDVS 828
:| | | :| | | :| | | :| | | :| | | :
RESULT 7
GCSR_MOUSE STANDARD; PRT; 837 AA.
ID GCSR_MOUSE AC P40223;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R).
GN CSF3R Or CSFGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90235283; PubMed=2158861;
RA Fukunaga R., Ishizaka-Ikeda E., Seto Y., Nagata S.;
RT "Expression cloning of a receptor for murine granulocyte colony-
RT stimulating factor.";
RL Cell 61:341-350(1990).
RN [2]
RP STRUCTURE BY NMR OF 225-333.
RX MEDLINE=97331327; PubMed=9187659;
RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
RT "Solution structure of an extracellular domain containing the wsxws
RT motif of the granulocyte colony-stimulating factor receptor and its
RT interaction with ligand.";
RL Nat. Struct. Biol. 4:498-504(1997).
CC -!- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
CC ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
CC THE CELL SURFACE.
CC -!- SUBUNIT: DIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
CC EMBL; M58288; AAA37673.1; .
DR PIR; A34898; A34898.
DR PDB; 1GCF; 22-OCT-97.
DR PDB; 1CTO; 22-OCT-97.
DR MGD; MGI:1339755; Csf3r.
DR InterPro; IPR002996; CR1A.
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DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat; 3D-structure.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 837 GRANULOCYTE COLONY STIMULATING FACTOR
FT RECEPTOR.
FT DOMAIN 26 626 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 627 650 POTENTIAL.
FT DOMAIN 651 837 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 118 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 122 228 FIBRONECTIN TYPE-III 1.
FT DOMAIN 229 333 FIBRONECTIN TYPE-III 2.
FT DOMAIN 334 431 FIBRONECTIN TYPE-III 3.
FT DOMAIN 432 528 FIBRONECTIN TYPE-III 4.
FT DOMAIN 529 624 FIBRONECTIN TYPE-III 5.
FT DISULFID 132 143 BY SIMILARITY.
FT DISULFID 249 296 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 837 AA; 93406 MW; 42295E989E2C8531 CRC64;

Query Match 5.0%; Score 313; DB 1; Length 837;
Best Local Similarity 20.0%; Pred. No. 2e-13;
Matches 183; Conservative 125; Mismatches 311; Indels 298; Gaps 40;

QY 337 PPKILTSVGSNVSEHC-IYKKENKI VPSKEIVVMNLAEKIPQSQYDVVSD--HYSKVTF 393
|| : | | | | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 33 PP--VVRLGDPVLASCTISPNC SKLDQQA KILWRLQDEPIOPGDRQHLPDGTQESLITL 90
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 394 FNLNETKPRGKFTY-----DAVYCCNEHECHRYAEIYVIDVNINIS CETDGYLT KMT C 447
:| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 91 PHLNYTQ---AFLFCLVPWEDSVQLLDQAELHAGIPPA----SPSNLSCLMHLTNSLVC 143
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 448 RWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIHPISEPKDCYQLQSDGFYECIFQP----- 502
:| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 144 QWEPGPETHLPTFSFI-LKFSR SR-----ADCYQGD TIDPCVAKKRQNNC 187
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 503 -----IFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPPSSVKAETINI----- 551
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 188 SIPRKNLLLYQYMAIWQAENMLGSSSEPKCLDPMDVVKLEPPMLQALDIGPDVVSHQP 247
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 552 GLLKISWEKPVFPENNL--QFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPVPDLCA---- 605
| | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 248 GCLWSW-KPWKPSYMEQECELRYQPQLKGANWTL--VFHLPSSKQDF---ELCGLHQA 301
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 606 -VYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEK----- 658
|| :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 302 PVYTLQMR CIRSSLPGFWSPWS-PG----LQLRPTMKAP----TIRLDTWCQKKQLDPGT 352
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 659 -NVTLLWKPLMKNDLSLSVQRYVINHHTS-----CNGTWSEDVGNHTKFTFLWTEQ 708
:| | | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 353 VSVQLFWKPTPLQEDSGQIQGYLLSWNSPDHQGDILHCNTT-----QLSCIFLLPSE 405
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 709 AHTVTVLAINSIGASVANFLTFSWPMKSVNIVQSLSAYPLNSSCVIVSW---ILSPSDY 765
| | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 406 AQNVTLVAYNKAGTSSPT---TVVFL ENEGPAVTGLHAMAQDLNTIWDWEAPSLLPQGY 462
:| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 766 KLMYFIIEWK----NLNEDGEIKWLRISSSVKKYYIHDHFIP IEKYQFSLYPIFMEGVGK 821
```

```
Db 463 -----LIEWEMSSPSYNNYSKSWIEPNNGNITGILLKDNINPFQLYRITVAPLYPGIVGP 517
QY 822 PKIINSFT-----
Db 518 PNVVTFAGERAPPAPALHLKHVGTWTAQLEWVPEAPRLGMIPLTHYTIWFADAGHSF 577
QY 830 -----QDDIEKHQSDAGLY-----VIVPV 848
Db 578 SVTLNISLHDFVLKLEPASLVHYVLMATSRAGSTNSTGLTLRTLDPSDLNIFLGILCLV 637
QY 849 IISSSILLGTLTLLISHORMKKLFWEDVPNPKNCWSAQGLNFQKPTFEHLFIKHTASVTC 908
Db 638 LLSTTCVV--TWLCKRRGKTSFWSVDVDPDAHSSLSWL-----674
QY 909 GPLLLEPETISEDISVDTSWKNKDEMMPPTVVSLSTTDLEKGSVCIS-DQFNSVNFs-- 965
Db 675 -PTIMEET---FQLPSFW-----DSSVPSITKITELEEDKKPTHWDSESSGNGSLP 722
QY 966 -----EAGTEVTYEDESQRQPFVKYATLISNKPSETGEE-----Q 1002
Db 723 ALVQAVVLQDPREIS---NOSQP-----PSRTGDQVLYGOVLESPTSPOGVM 766
QY 1003 GLINSSVTKCFSSKNSPLKDFSNSWEIEAQAFFILSDQHPN-----IISPHLTFS--- 1054
Db 767 QYIRSDSTQPLLGCTPSPKSYENIWFHSRPOETFV--PQPPNQEDDCVFGPPDFPFLFQ 824
QY 1055 ----EGLDELLKLEGNF 1067
Db 825 GLQVHGVEE---QGGF 837

RESULT 8
LIFR_HUMAN
ID LIFR_HUMAN STANDARD; PRT; 1097 AA.
AC P42702;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukemia inhibitory factor receptor precursor (LIF-R).
GN LIFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92007727; PubMed=1915266;
RA Gearing D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,
RA King J., Price V., Cosman D., Beckmann M.P.;
RT "Leukemia inhibitory factor receptor is structurally related to the
RT IL-6 signal transducer, gp130.";
RL EMBO J. 10:2839-2848(1991).
CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
CC -!- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
CC MEMBRANE-BOUND AND A SECRETED FORM.
CC -!- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
CC MAY ARISE BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
```

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CC EMBL; X61615; CAA43805.1; -.
DR MIM; 151443; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SMO0060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Alternative splicing; Repeat.
FT SIGNAL 1 44 POTENTIAL.
FT CHAIN 45 1097 LEUKEMIA INHIBITORY FACTOR RECEPTOR.
FT DOMAIN 45 833 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 834 858 POTENTIAL.
FT DOMAIN 859 1097 CYTOPLASMIC (POTENTIAL).
FT DISULFID 55 65 BY SIMILARITY.
FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 572 572 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 652 652 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 729 729 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 787 787 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1097 AA; 123742 MW; C8602897E359FCE5 CRC64;

Query Match 4.7%; Score 294.5; DB 1; Length 1097;
Best Local Similarity 19.2%; Pred. No. 5.3e-12;
Matches 215; Conservative 179; Mismatches 385; Indels 339; Gaps 52;

QY 161 LLYVLPEVLEDSPLVPQKGSFQMVHC-----NCS-----VHECC----- 194
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 35 LLYLMNQVNSQ-----KKGAPHDLKCVTNLNQVWNCWKAPSGTGRGTDYEVCIENRSRS 89
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
QY 195 -----ECLVFPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMVKPDPPPLGLHMEIT- 248
: : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : :
Db 90 CYQLERTSIKIPALSHGDYEITINSLHDFGSGTSKFTLNEQVNSLI-PDTPEILNLSADF 148
| : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 249 DDGNLKLISWSSPPLVPFPPLQYQVKYSENSTVIR---EADKIVSATSLI----- 294
| : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 149 STSTLYLKWNRGVS-FPHRSNVIW---EIKVLRKESMELVKLVTHNTTLNGKDTLHHWS 204
| : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 295 --VDSILPGSSYEVOVR---GKRLDGPGLSDWSTPRVFT---TQDVYFPPKILTSVG 345
| : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 205 WASDMPLECAIHFEIRCYIDNLHFGLEWSDWSPVKNISWIPDSQTKVFPQDKVILVG 264
| : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 346 SNVSFHCIIYKKENKIVPSKEIYVWWMNLAEKIPQSOYDVV---SDHVSKVTFNLTNETKPR 402
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 265 SDITFCV-----SQEKV-----LSALIGHTNCPLIHLDDGENVA-IKIRNISVSASS 310
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 403 GKFTYDAVYCCNEHECHRYAEALYVIDVNMNINISCTDGYLTGKMTCRWSTSTIQSLA---E 459
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 311 GT---NVVFTTEDNIFGTIVFAGYPPDTPQQLNCETHD-LKEIICSWNPGRVTALVGPR 366
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 460 STLQLRYHRSSLYCSDIPSIHPISEPKCYLQSDGFYECIFQPIFLLSGYTMWIRINHSL 519
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 367 TSYTLVESFSGKYVRLKRAEAPTNE-----YQLLFQMLPNQEIYNETLNAHNP 416
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 520 GSLDSPPTCVLPDPSVVKPLPPSSVKAETINIGLLKISWEKP-----VFPEP 566
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
```

Db 417 GRSQSTILVNITEKVY-PHTPTSEKVK-DINSTAVKLSWHLPGNFAKINFLCEIEIKKSN 474

QY 567 NLQFQIRYGLSGKEVQWKMEYVDYDAKSKSVSLPVPDLCVAVYAVQVRCKRLDGLGYWSNWS 626

Db 475 SVQEQRNVITKGE-----NSSYLVALDKLNPYTLTYFRIRCS-TETFWKWSKWS 523

QY 627 NPAYTVVMDIKVPMRGPEFRIINGDTMKKEKNVTLLWKPLMKNDLSCSVQRYVINHHTS 686

Db 524 NKKQHLTTEAS-PSKGPDTREWSSD----GKNLIYWKPLPINEA----NGKILSYNVS 574

QY 687 CNG-----TWSEBDVGNHTKFTFLWTEQAHTVTVVLAINSIGASVANFNLTFSWPMSKVNIIV 741

Db 575 CSSDEETQSLSEIPDPQHKAEIRLDKNDYIISVAKNSVGSSPPSKIASMEIPNDLKE 634

QY 742 QLSAYPLNSSCVIVSWILSPS---DYKLMYFIIEWKN--LNEDGEIKWLRI-SSSVKKY 795

Db 635 QVVG-----GKGILLTWHYDPNMTCDY-----VIKWCNSSRSEPCMLDMRKVPSNSTETV 685

QY 796 YIHDHFIPIEKYQFSLYPIFMEG-----VG-----KPKIINSFTQDD----- 832

Db 686 IESDEFPRGIRYNEFFLYGCRNQYQLLRSMIGYIEELAPIVAPNFTVEDTSADSILVKWE 745

QY 833 -----IEKHQSD----- 839

Db 746 DIPVEELRGLRGLYFYFGKGERDTSKMRVLESGRSDIKVKNITDISQKTLRIADLQGT 805

QY 840 -----AGLYVI-----VPIISSILLGLTLLISHQR--M 867

Db 806 SYHLVLRAYTDGSGVPEKSMYVVTKENSVGLIIAILIPVAVAVIVGVVTSILCYRKREWI 865

QY 868 KKLFWEDVPNPKNCSWAQLNFQK-----PETFEHLFIKHTASVTCGPLL 912

Db 866 KETFPYDIPNENC--KALQFQKSVCESSALKTLEMNPTPNVVELETRSAF--PKI 920

QY 913 LEPETISEDISVDTSWKNKDEMPTTVVLSLLSTDLEKGSVC---ISDQFNSVNFSEAG 969

Db 921 EDTEIIS---PVAERPEDRSDAEPENHVVV-----SYCPPIIEEIPNPADEAGG 968

QY 970 T-EVTYED-ESQRQPFVKYATLISNKPSETGEEQGL-----INSSVTKCFS- 1014

Db 969 TAQVIYIDVQSMYQP-----QAKPEEEQENDPVGGAGYKPKQMPLPINSTVEDIAAE 1019

QY 1015 ---SKNSPLKDSFSNSSWEIEAQAFFILSDQHPNIISP 1049

Db 1020 EDLDKTAGYRPOANVTW-----NLVSP 1042

RESULT 9

GCSR_HUMAN

ID GCSR_HUMAN STANDARD; PRT; 836 AA.

AC Q99062;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R)

DE (CD114 antigen).

GN CSF3R OR GCSFR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=91079757; PubMed=2147944;

RA Larsen A., Davis T., Curtis B.M., Gimpel S., Sims J.E., Cosman D., Park L., Sorensen E., March C.J., Smith C.A.;

RT "Expression cloning of a human granulocyte colony-stimulating factor receptor: a structural mosaic of hematopoietin receptor, immunoglobulin, and fibronectin domains.";

RL J. Exp. Med. 172:1559-1570(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=91062348; PubMed=1701053;

RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;

RT "Three different mRNAs encoding human granulocyte colony-stimulating factor receptor.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=92091782; PubMed=1530796;

RA Seto Y., Fukunaga R., Nagata S.;

RT "Chromosomal gene organization of the human granulocyte colony-stimulating factor receptor.";

RL J. Immunol. 148:259-266(1992).

RN [4]

RP DOMAINS STRUCTURE.

RX MEDLINE=92007729; PubMed=1717255;

RA Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;

RT "Functional domains of the granulocyte colony-stimulating factor receptor.";

RL EMBO J. 10:2855-2865(1991).

RN [5]

RP STRUCTURE BY NMR OF 227-334.

RX MEDLINE=97331327; PubMed=9187659;

RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;

RT "Solution structure of an extracellular domain containing the WSXWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand.";

RL Nat. Struct. Biol. 4:498-503(1997).

RN [6]

RP 3D-STRUCTURE MODELING OF 125-331.

RX MEDLINE=98037802; PubMed=9368043;

RA Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;

RT "Identification of a ligand-binding site on the granulocyte colony-stimulating factor receptor by molecular modeling and mutagenesis.";

RL J. Biol. Chem. 272:29735-29741(1997).

CC -|- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT THE CELL SURFACE.

CC -|- SUBUNIT: DIMER (PROBABLE).

CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM, WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM OF THE RECEPTOR.

CC -|- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; GCSFR-1 (SHOWN HERE), GCSFR-2, GCSFR-3 AND GCSFR-4/D7; SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.

CC -|- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES. THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.

CC -|- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME; ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).

CC -|- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -|- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -|- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -|- DATABASE: NAME=PROW; NOTE=CD gulde CD114 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".

CC -----

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CC -----

CC EMBL; X55721; CAA39253.1; -.

DR EMBL; X55720; CAA39252.1; -.

DR EMBL; S71484; AAB20660.1; -.

DR EMBL; M59818; AAA63176.1; -.

DR EMBL; M59819; AAA63177.1; -.

DR EMBL; M59820; AAA63178.1; -.

DR PIR; JH0329; JH0329.

CC LOW AFFINITY.
CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
CC EMBL: U64199; AAB36676.1; -.
CC HSSP: P40189; 1BQU.
CC MGD: MGI:1270861; IL12rb2.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003961; FN.III.
CC InterPro: IPR003962; FN.III_repeat.
CC InterPro: IPR003529; Hematopo_receptor_L_F2.
CC Pfam: PF00041; fn3; 4.
CC PRINTS: PR00014; FNTYPEIII.
CC SMART: SM00060; FN3; 3.
CC PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 20
FT CHAIN 21 874
FT DOMAIN 21 639
FT TRANSMEM 640 656
FT DOMAIN 657 874
FT DOMAIN 137 230
FT DOMAIN 240 322
FT DOMAIN 436 523
FT DOMAIN 534 622
FT CARBOHYD 48 48
FT CARBOHYD 101 101
FT CARBOHYD 114 114
FT CARBOHYD 142 142
FT CARBOHYD 151 151
FT CARBOHYD 169 169
FT CARBOHYD 179 179
FT CARBOHYD 224 224
FT CARBOHYD 252 252
FT CARBOHYD 279 279
FT CARBOHYD 287 287
FT CARBOHYD 323 323
FT CARBOHYD 391 391
FT CARBOHYD 495 495
SQ SEQUENCE 874 AA; 98196 MW; 582E4D21BF1FBD67 CRC64;

Query Match 3.5%; Score 220; DB 1; Length 874;
Best Local Similarity 20.3%; Pred. No. 4.2e-07;
Matches 166; Conservative 95; Mismatches 286; Indels 270; Gaps 42;

QY 433 NISCTDGYLTMTCRWSTSTIOSLAES-TLQRYHRSSLYCSDIPSIHPSEPKDCYLQ 491
Db 142 NISCVQEGENGTVACSWNSGKVTYIKNTYTLQLS-GPNNLTCQ-----KQCF-- 187

QY 492 SDGFYEC-----IFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKLPSPSVK 544
Db 188 SDNRQNRDLGINSPLDAESRFIVRTAINDLGNSSSLPHTFTFLDIVIPLPPWDIR 247

QY 545 AEITINIGLLKIS-----WE-KPVFPENNLFQIRYGLSCKEVQWKMEYVDKSKSV 596
Db 248 -----INFLNAGSGRGLQWEDEGQVVLNQLRYQPLNSTS-----WNMVNATNAKGG-- 294

QY 597 SLVPDDL--CAVYAVQVRCK-RLDGLGYWSNWSNPAYTVVMDIKVPMRGP-----EFWRII 649
Db 295 -YDLRLRPFTEYEFQISSKULHLSG-GSWSNWSESLRT-----RTPEEPVGILDIW-YM 346

QY 650 NGDTMKKEKNVTLLWKPLMKNDLSLCVQRYVINHHHTSCNGTWSDEVGNHHTKFTFLWTE-- 707
Db 347 KQIDYDRQOISLFWKSLNPSEARGKILHYQVTLQEVTKKTLQNTTRHTS-----WTRVI 402

QY 708 ---QAHTVTVLAINSIGASVANFNLTFSWPMSKVNIY-----QSLSAYPLNSSCV 754
Db 403 PRGTAWTASVSAANSKGASAP-----THINIVDLCGTGLLAPHQVSAKSENMDNI 452

QY 755 IVSWILSP--SDYKLMYFIENKLNEDGEI-----KWLR-----ISSSVKKYYI 797
Db 453 LVTW--QPPKKADSAVREYIVEMRAL-QPGSITKFPFHWLRIPPDNMSALISENIKPYIC 509

QY 798 HD-----HFIPI-----EKYQ----- 808
Db 510 YEIRVHALSESQGGCISIRGDSKHKAPVSGPHITAITEKKERLFISWTHIPPEQRCIL 569

QY 809 -FSLYPIFMIEGVGPKII-----NSFTQDDIEKH----- 836
Db 570 HYRIYWKERDSTAQPELCEIQYRRSQNSHPISLSLOPRVTVYVLMTAVTAAGESPQGNERE 629

QY 837 ---QSDAGLYVIVPVISSSILLGLTLLISHQRMK-----KLEW--EDVPNPKNCW 883
Db 630 FCPQGANWKAFAVISSICIAIITVGTFSIRYFRQKAFLLSTLKPQWYSRTIPDPANSTW 689

QY 884 AQGLNEQKPEFTEHFLFIKHTASVTGCGPLLLLEPETISEDISVDTSWKNKDEMMPTTVVSL 943
Db 690 VK-----KY-----PILEEKIQLPD-NLLMAWPTPEPEPLIIEVL 726

QY 944 -----STDLKSGVCSISDQFNSVNFSEAEGETEVTYEDESQRQP 982
Db 727 YHMIPVVRQPYFVKRGGFGYSTSKQDAMYIANPQATGTLTAETROLVNLVKVLESRD 786

QY 983 FVKYATLIS-----NSKPSETGEEGLINSSVTCKFSSKNKSPKDSFNSSSWEIEAQ- 1034
Db 787 DSKLANLTSPLTVPVNYLPS---HEGVLPNIEDLSPHEADP-----TDSFDLEHQH 836

QY 1035 ---AFFILSDQHPNII-SPHLTFSE---GLDELLKLE 1064
Db 837 ISLSIFASSSLRPLIFGGERLTLDRLKMGYDSLMSNE 873

RESULT 14
PRLR_CHICK
ID PRLR_CHICK STANDARD; PRT; 831 AA.
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE prolactin receptor precursor (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-Kidney;
RX MEDLINE=93075121; Pubmed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RT the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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DR EMBL; D13154; BAA02439.1; -.
DR PIR; JQ1655; JQ1655.
DR HSSP; P14787; 1AN3.
DR InterPro; IPR002996; CRLA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 831 PROLACTIN RECEPTOR.
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 439 459 POTENTIAL.
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 1C4E7591DCADBE9 CRC64;

Query Match 3.3%; Score 209.5; DB 1; Length 831;
Best Local Similarity 20.4%; Pred. No. 2e-06;
Matches 174; Conservative 127; Mismatches 291; Indels 263; Gaps 46;

QY 476 IPSIHPISEPKCYLQSDGFYECIFQPIFLSG-----YTMWIRINHS 519
DB 56 LPTNYTLFYSKD---SEEEIYEC---POYRTSGPNSCYFNKNHTSPWTFNITVTATNEI 109

QY 520 GSLDSPPTCVLPDSVVKPLPPSSVKAEL--TINIGLLKISWEKVPFPE---NNL-QFOIR 573
DB 110 GSNSSDPQYVDVTSIVQPGSPVNLTLTKRGSANIMYLWAKWSPPLLADASSNHLHYELR 169

QY 574 YGLSGKEVQKMYEVYDAKSKSVSLPVPDLCAV-----YAVQVRCKRLDGLGYWSNW 625
DB 170 IKPEKE-EW-----ETISVGVTQCKINRLNAGMRYVQVRC-TLDP-GEWSEW 216

QY 626 SNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNDLCSVQRYVINHHT 685
DB 217 SSERHILIPSGOSP---PEKPTIIKCRSPEKE-TFTCWKPKGLDG-----GHPT 261

QY 686 SCNGTWSED-----VGNHT-----KFTFLWTEQAHTVTVLAINSIGASVAN- 726
DB 262 NYTLLYSKEGEQVEQVCEPDYRTAGPNSCYFDKKHTSFTW--IYNITVRATNEMGSNSDP 319

QY 727 --FNLTF-SWPMKSNVIVQSLASAYPLN-SSCVIVSWILSP-SDYKLMYFIIEW--KNLNE 779
DB 320 HYVDVTYIVQDPDPVNVNLTLEKK-PINKRPVYLVTWSPPLADVRSGWLTLEYELRLKPE 378

QY 780 DGEIKWLRISSSKVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKH--- 836
DB 379 EGE-EWETIFVGQQTQYKMFSLNPGKKYIIQIH-----CKPDHGSWSEWSSENYIQI 430

QY 837 -----QSDAGLYVIVPVIISSSILLG-TLLTSHQRMKLFWEDEVNPKNCSWAQGLNFQ 890
DB 431 PNDFRVKDMIVIVGLVLSLCLIMSWTLKGYRMITFMLPPVPGPK-----IKGIDTH 486

QY 891 KPET-----FEHLFIKH-----TASVT- 907
DB 487 LLETGKSEELLSALGCHGLPPTSDCEELLIEYLEVEDSEDOQLMPSHDNGHPSKNAKTR 546

QY 908 -----C-GPLL-----EPETISEDISVDTSWKNKDEMPTT 938
DB 547 KETDSDSGRGSCDSPSLSEKRETCALPPVLTQEVDRDVQEKKAARSWET--QYVASE 604

QY 939 VVSLLTSTDLEKGSVCISDQF-NS-----VNFSEAEGETEVTYEDESQR 980
DB 605 RKALLSNSESAKSSTWPAVQLPNSQPPMFAYHSIVDAHKITLNTTNTNVAALVDEEEH 664

QY 981 QPFVKYATLISNSKPSSETGEEQGL-----INSSVTCKFSSKNSPLKDSFSSWEIEAQ 1034
DB 665 QSQCSTLTETIPGEMEKQ-GEMENLHSHKTEQTAQVKQNRNRLPFLDAAALMDYVEVHK- 722

QY 1035 AFFILSDQHPNITISPHLTFSEGLDELLKLEGNFPEENNDKKSIV-----YLGVTSIK 1086
DB 723 --VIRQDEEPAVLKHK-----KENSGKIEKYTISGASKEYTKVSTVM 762

QY 1087 KRESGVLLTFDKSRVSCPPFA---PCLFTDIRVLQDSCSHFVENNIN-----LG 1131
DB 763 DHNILVLPD-SRVP-HTPASQEPAKETSQSLQQGQ---VEKNMSYCLTAPSDCKRETG 816

QY 1132 TSSKKTTFASYMPOFQ 1146
DB 817 GSEYMDPSSFMPSFK 831

RESULT 15
PRLR_MELGA
ID PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (TPRLR).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo."
RL Biol. Reprod. 55:1081-1090(1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE=Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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DR EMBL; L76587; AAB01544.1; -.
DR EMBL; U22947; AAA75038.1; -.

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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:20:00 ; Search time 54.95 Seconds
(without alignments)
2037.199 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVVLLHWEFIYVIT.....QTCSTQTHKIMENKMCDLTV 1165
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-711
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4784.5	76.5	1162	2 PC4184	leptin receptor, O
2	4766.5	76.2	1162	2 S68438	leptin receptor, s
3	3793	60.6	900	2 S68440	leptin receptor, s
4	3785	60.5	892	2 S68439	leptin receptor, s
5	3785	60.5	894	2 S68437	leptin receptor, s
6	3729	59.6	895	2 S74225	leptin receptor, i
7	3340	53.4	805	2 S68441	leptin receptor, s
8	366	5.9	917	2 I49699	glycoprotein 130 -
9	345.5	5.5	918	2 A36337	membrane glycoprot
10	339.5	5.4	918	2 A44257	interleukin-6 sign
11	313	5.0	837	2 A34898	granulocyte colony
12	294.5	4.7	1097	2 S17308	leukemia inhibitor
13	288.5	4.6	863	2 C38252	granulocyte colony
14	284	4.5	783	2 JH0329	granulocyte colony
15	281.5	4.5	1092	2 JX0312	differentiation-st
16	277	4.4	771	2 B38252	granulocyte colony
17	251.5	4.0	2302	2 T14328	protein-tyrosine-p
18	220	3.5	830	2 I50455	prolactin receptor
19	209.5	3.3	831	2 JQ1655	prolactin receptor
20	191.5	3.1	5805	2 S20901	titin - rabbit (fr
21	188	3.0	26926	1 I38344	titin, cardiac mus
22	182.5	2.9	1471	2 T19506	hypothetical prote
23	177	2.8	2481	2 A43908	fibronectin - Afri
24	174	2.8	1375	2 T13822	frazzled gene prot
25	172	2.8	1896	2 T08851	Down syndrome cell
26	170	2.7	1232	2 T43027	neural cell adhesi
27	169.5	2.7	1443	2 I50600	neogenin - chicken
28	166.5	2.7	2029	1 TDFFLK	protein-tyrosine-p
29	166	2.7	3488	2 T34418	hypothetical prote

30	165	2.6	630	2 I51086	prolactin receptor
31	165	2.6	1526	2 T13823	frazzled gene prot
32	160	2.6	1197	2 T30581	neural cell adhesi
33	159	2.5	2340	2 I48310	kinase-related pro
34	158	2.5	1825	2 C88400	protein H19M22.1 [
35	158	2.5	1825	2 T32828	hypothetical prote
36	158	2.5	2338	2 I73957	kinase-related pro
37	156	2.5	1000	2 I46521	titin - rabbit (fr
38	154.5	2.5	2386	1 FNHU	fibronectin precur
39	153.5	2.5	440	2 JL0144	interleukin-6 rece
40	153.5	2.5	460	2 JL0145	interleukin-6 rece
41	153.5	2.5	610	2 A36116	prolactin receptor
42	150.5	2.4	310	2 A29884	prolactin receptor
43	150.5	2.4	412	2 A41070	prolactin receptor
44	150.5	2.4	5005	2 F82884	hypothetical prote
45	148.5	2.4	610	2 A34631	lactogen receptor

ALIGNMENTS

RESULT 1
PC4184
leptin receptor, Ob-Rb - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000
C;Accession: JC4895; JC4896; JC4897; PC4184; JC4797
R;Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Ta
Biochem. Biophys. Res. Commun. 225, 75-83, 1996
A;Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi
A;Reference number: JC4895; MUID:96332408
A;Accession: JC4895
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1162 <TA2>
A;Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BAA12831.1; PID:d1013515; PID:g15
A;Accession: JC4896
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-889, 'RADTL' <TA2>
A;Cross-references: DDBJ:D85557
A;Accession: JC4897
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-796, 'G', 1157-1158, 'TVLLN' <TA3>
A;Cross-references: DDBJ:D85559
R;Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 224, 597-604, 1996
A;Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)
A;Reference number: PC4184; MUID:96295531
A;Accession: PC4184
A;Molecule type: mRNA
A;Residues: 840-1162 <IID>
A;Cross-references: DDBJ:D84550
R;Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 222, 19-26, 1996
A;Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker f
A;Reference number: JC4797; MUID:96212906
A;Accession: JC4797
A;Molecule type: mRNA
A;Residues: 1-889, 'RADTL' <II2>
A;Cross-references: DDBJ:D84125; NID:g1374707; PIDN:BAA12230.1; PID:g1374708
A;Experimental source: adipose cell
C;Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa
C;Genetics:
A;Gene: fa
C;Keywords: appetite; transmembrane protein
F;840-860/Domain: transmembrane #status predicted <TMM>
F;861-1162/Domain: intracellular #status predicted <INT>

Query Match 76.5%; Score 4784.5; DB 2; Length 1162;
Best Local Similarity 75.6%; Pred. No. 6.5e-303;

Matches		882; Conservative	118; Mismatches	161; Indels	5; Gaps
Qy	1	MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS	60		
Db	1	MTQCKFYVLLHWEFLYVITALNLAYPTSPWRFKLCFAPBSTDDSFSPAGVPNNTSSL	60		
Qy	61	NGHYETAPEPKFNSSGTHFSLNSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120		
Db	61	KGASEALVEAKFNSTGIYVSELSKTFHCCFGNEQGQNCALTGNTGKTLASVVKPLVF	120		
Qy	121	QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPEVLEDSPLVPQKGS	180		
Db	121	RQLGVNWDIECWMKGDLTFLFICHMEPLLLKNPFKNYDSKVHLLYDLPEVIDDLPLPLKDS	180		
Qy	181	FQMVHCNCSVHECCECLVPVPTAKINDTLLMCLKITSGGVIFQSPMSVQPINMVKPDPP	240		
Db	181	FQTQCNCYSVRE-CECHVPVPRAKVNYALLMYLEITSAGVSFQSPMSLQPLMLVVKPDPP	239		
Qy	241	LGLHMEITDDGNLKSISWSSPPLVPFPFLOQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300		
Db	240	LGLRMEVTDGNLKSISWDSQTKAPFPLOQYQVKYLENS-TIVREAAEIVSDTSLLVDSVLP	298		
Qy	301	GSSYEQVRGKRDLGPGIWSDMSTPRVFTTQDVYFPPKILTSVGSNVSFHCIIYKKENKI	360		
Db	299	GSSYEQVRSKRDLGSGVWSDSLQFLTQDVMYFPPKILTSVGSNASFCCLYKKNENQT	358		
Qy	361	VPSKEIVWMNLAEKIPQSQYDVVDHVSKVTFNFLNETKPRGKFTYDAVYCCNEHECHH	420		
Db	359	ISSKQIVWMNLAEKIPETQYNTVSDHISKVTFSNLKAATPRGKFTYDAVYCCNEQACHH	418		
Qy	421	RYAELYVIDVNNISCETDGYLTMTKTCRWSTSTIQSLAESTLQLRYHRSLSYCS DIPSIH	480		
Db	419	RYAELYVIDVNNISCETDGYLTMTKTCRWSPSTIQSLVGSVQLRYHRSLYCPDNPSIR	478		
Qy	481	PISEPKDCYLOSDFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP	540		
Db	479	PTSELKNCVLQTDGFYECVFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP	538		
Qy	541	SSVKAELITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSILPV	600		
Db	539	SNVKAELITINTGLLKVSWEKVPFPENNLOFQIRYGLNGKEIQWKTHEVFDAKSKSASLPV	598		
Qy	601	PDLCAYYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660		
Db	599	SDLCAVYVQVRCRRRLDGLGYSNWSNPAYTLVMDVKVPMRGPEFWRIMDGDITKKERNV	658		
Qy	661	TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSQVGNHTKFTFLWTEQAHTVTVLAINSI	720		
Db	659	TLLWKPLMKNDSLCSVRRYVYVVKHRTAHNGTWSQVGNQTNLTFLWAESHTVTVLAINSI	718		
Qy	721	GASVANFNLTESWPMSKVNIQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIIEWKNLNE	780		
Db	719	GASLVNFNLTFSWPMSKVNAVQSLASAYPLSSSCVILSWILSPNDYSLLYLVIEWKNLNDD	778		
Qy	781	GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPFMEGVGKPKIINFTQDDIEKHQSDA	840		
Db	779	DGMKWLRIPSNVNKYYIHDNFPIPIEKYQFSLYPVFMGVGKPKIINGFTKDDIAKQQND	838		
Qy	841	GLYVIVPVISSSILLGLTLISHQRMKLFWEDVNPKNCSWAQGLNFQKPETFEHLFI	900		
Db	839	GLYVIVPIIISSCVLLGLTLISHQRMKLFWDVNPKNCSWAQGLNFQKPETFEHLFT	898		
Qy	901	KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTT-DLEKGSVCISDQF	959		
Db	899	KHAESVIFGPLLLEPEPVSEISVDTAWNKDDEMVPAAVMSLLTTPDSTRGSICISDQC	958		
Qy	960	NSVNFSEAEGTEVTYDEDSQROPFVKYATLISNKSPPSETGEEQGLINSSVTKCFSSKNSP	1019		
Db	959	NSANFSGAQTQGTCEDECQSQSPVKYATLVSNVKTVETDEEQGAIHSSVSQCIARKHSP	1018		
Qy	1020	LKDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNKKSIYY	1079		
Db	1019	LROSFSNSWEIEAQAFFLLSDHPPNVISPQLSFS-GLDELLELEGNFPEENHGEKSVYY	1077		

Qy	1080	LGVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFA	1139		
Db	1078	LGVSNGKRENDMLLTDEAGVLCPPFAHCLFSDIRILQESCSEHFVENNLNLTSG-KNEV	1136		
Qy	1140	SYMPQFQTCSTQTHKIMENKMCDLTV	1165		
Db	1137	PYMPQFQSCSTHSHKIIENKMCDLTV	1162		
RESULT 2					
S68438					
leptin receptor, splice form Ob-Rb - mouse					
C;Species: Mus musculus (house mouse)					
C;Date: 17-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000					
C;Accession: S68438; S68441					
R;Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Nature 379, 632-635, 1996					
A;Title: Abnormal splicing of the leptin receptor in diabetic mice.					
A;Reference number: S68437; MUID:96231997					
A;Accession: S68438					
A;Status: nucleic acid sequence not shown					
A;Molecule type: mRNA					
A;Residues: 664-1162 <LEE1>					
A;Cross-references: EMBL:U49107; NID:g1195486; PIDN:AAC52421.1; PID:g1195487					
A;Experimental source: splice form Rb; tissue hypothalamus					
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996					
A;Note: only a part of the translation is shown					
A;Accession: S68441					
A;Status: nucleic acid sequence not shown; translation not shown					
A;Molecule type: mRNA					
A;Residues: 1-796,'GMCTVLFMD' <LEE2>					
A;Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493					
A;Experimental source: splice form Re; tissue hypothalamus					
A;Note: this sequence was submitted to the EMBL Data Library, February 1996					
A;Note: this sequence from splice form Re is included to produce a complete sequence					
C;Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR: C;Genetics:					
C;Gene: Ob-Rb					
C;Keywords: alternative splicing; appetite					

Query Match	76.2%;	Score	4766.5;	DB 2;	Length	1162;
Best Local Similarity	75.4%;	Pred.	No. 9.6e-302;			
Matches	879;	Conservative	115;	Mismatches	167;	Indels 5; Gaps 5;

Qy	1	MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS	60		
Db	1	MMQKFFVLLHWEFLYVIAALNLAYPISPWKFLFCGPPNTDDSFSPAGAPNNASAL	60		
Qy	61	NGHYETAPEPKFNSSGTHFSLNSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120		
Db	61	KGASEAIVEAKFNSSGIYVPELSKTVFHCCFGNEQGQNCALTDTNTEGKTLASVVKASVF	120		
Qy	121	QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPEVLEDSPLVPQKGS	180		
Db	121	RQLGVNWDIECWMKGDLTFLFICHMEPLPKNPFKNYDSKVHLLYDLPEVIDDSPLPLKDS	180		
Qy	181	FQMVHCNCSVHECCECLVPVPTAKINDTLLMCLKITSGGVIFQSPMSVQPINMVKPDPP	240		
Db	181	FQTQCNCSLRG-CECHVPVPRAKLNLYALLMYLEITSAGVSFQSPMSLQPLMLVVKPDPP	239		
Qy	241	LGLHMEITDDGNLKSISWSSPPLVPFPFLOQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300		
Db	240	LGLHMEVTDGNLKSISWDSQTMAPPFLQYQVKYLENS-TIVREAAEIVSATSLLVDSVLP	298		
Qy	301	GSSYEQVRGKRDLGPGIWSDMSTPRVFTTQDVYFPPKILTSVGSNVSFHCIIYKKENKI	360		
Db	299	GSSYEQVRSKRDLGSGVWSDMSSPQVFTTQDVVYFPPKILTSVGSNASFHCIIYKKNQOI	358		
Qy	361	VPSKEIVWMNLAEKIPQSQYDVVDHVSKVTFNFLNETKPRGKFTYDAVYCCNEHECHH	420		
Db	359	ISSKQIVWMNLAEKIPEIQYISIVSDRVSKVTFSNLKAATPRGKFTYDAVYCCNEQACHH	418		

QY	421	RYAELYVIDVNIINISCE	TGDLTKMTCRWSTSTIQSLAESTLQLR	YHRSSLYCSDIPS	480
Db	419	RYAELYVIDVNIINISCE	TGDLTKMTCRWSPSTIQSLVGSTVQLR	YHRSSLYCPDSPSIH	478
QY	481	PISEPKDCYLQSDGFYEC	IFQPIFLLSGYTMWIRINHS	LSGLDSPPTCVLPDSVVKPLPP	540
Db	479	PTSEPKNCVLQDGFYECV	FQPIFLLSGYTMWIRINHS	LSGLDSPPTCVLPDSVVKPLPP	538
QY	541	SSVKAETINIGLLKISWE	KVPFVPENNLFQIRYGLSGKEVQW	KMEYVDKSKSVSLPV	600
Db	539	SNVKAETIVNTGLLKVSWE	KVPFVPENNLFQIRYGLSGKEIQW	KTHEVFDKSKSASLLV	598
QY	601	PDLCAVYAVQVRCKRLD	GLGYWSNWSNPAYTVVMDIKVPMRG	PEFWRIINGDTMKKEKNV	660
Db	599	SDLCAVYVQVRCRRLD	GLGYWSNWSNPAYTLVMDVQVPMRG	PEFWRKMDGDVTKKERNV	658
QY	661	TLLWKPLMKNDLSVQRY	VVINHHTSCNGTWSVDVGNHTKFT	FLWTEQAHTVTVLAINSI	720
Db	659	TLLWKPLTKNDLSVRRY	VVKHRTAHNGTWSVDVGNHTKFT	FLWTEPAHTVTVLAVNSL	718
QY	721	GASVANFNLTFSWPM	SKVNIQVQSLASAYPLNSSCVIVSW	ILSPSDYKLMYFII EWKNLNED	780
Db	719	GASLVNFNLTFSWPM	SKVSAVESLSAYPLSSSCVILSW	ILSPDDYSLLYLVIEWKILNED	778
QY	781	GEIKWLRISSSVKKYI	HDHFIPIEKYQFSLYPIFMEGV	GKPKIINSFTQDDIEKHQSDA	840
Db	779	DGMKWLRIPSNVKKFY	IHDNFIPIEKYQFSLYPVFM	EGVGKPKIINGFTKDAIDKQONDA	838
QY	841	GLYVIVPVIIS	SILLGLTLLISHQRMKKLFW	EDVNPKNCSWAQGLNFQKPF	FEHLFI 900
Db	839	GLYVIVPIIIS	CVLLGLTLLISHQRMKKLFW	DDVNPKNCSWAQGLNFQKPF	FEHLFT 898
QY	901	KHTASVTCGPLLEPET	ISEDIVDTSWKNKDEMPTTVVSL	STT-DLEKGSVCISDQF	959
Db	899	KHAESVIFGPLLEPEPI	SEISVDTAWKNKDEMVPAAW	SLLTTPDPRESSICISDQC	958
QY	960	NSVNFSEAE	TEVTYEDESQRQPFVKYATLIS	NKSPSETGEEQGLINSSVT	KCFSSKNSP 1019
Db	959	NSANFSGSQSTQVTC	EDCQRQPSVKYATLVSNDKLV	ETDEEQGFHSPVSNCLSSNHSP	1018
QY	1020	LKDSFNSWEIEA	QAFILSDQHPNIIISPHLTFSE	GLDELLKLEGNFPEENN	DKKSIYY 1079
Db	1019	LROFSFSSSWETE	QAFILSDQHPNIIISPHLTFSE	GLDELLKLEGNFPEENHREKSVCY	1077
QY	1080	LGVTSIKKRES	GVLLTDKSRVSCPPFAPCLFTD	IRVLQDSCSHFVENNIN	LGTSSKKTEFA 1139
Db	1078	LGVTSVNRRES	GVLLTGEAGILCTFPAQCLF	SDIRILQERC	SHFVENNLSLGTSG-ENFV 1136
QY	1140	SYMPQFQTCSTQ	THKIMENKMC	DLTV 1165	
Db	1137	PYMPQFQTCSTH	SHKIMENKMC	DLTV 1162	
RESULT	3				
S68440	leptin receptor, splice form Ob-Rd - mouse				
C:Species:	Mus musculus (house mouse)				
C:Date:	17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000				
C:Accession:	S68440				
R;Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; F					
Nature 379, 632-635, 1996					
A:Title:	Abnormal splicing of the leptin receptor in diabetic mice.				
A:Reference number:	S68437; MUID:96231997				
A:Accession:	S68440				
A>Status:	nucleic acid sequence not shown; translation not shown				
A:Molecule type:	mRNA				
A:Residues:	1-900 <LEE>				
A:Cross-references:	EMBL:U49109; NID:g1195490; PIDN:AAC52423.1; PID:g1195491				
A:Experimental source:	tissue hypothalamus				
A>Note:	the nucleotide sequence was submitted to the EMBL Data Library, February 1996				
C:Comment:	For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68				
C:Genetics:					

A:Gene: Ob-Rd							
C:Keywords: alternative splicing; appetite; transmembrane protein							
F:840-860/Domain: transmembrane #status predicted <TMM>							
Query Match		60.6%;	Score 3793;	DB 2;	Length 900;		
Best Local Similarity		76.8%;	Pred. No. 1.4e-238;				
Matches 691;		Conservative 83;	Mismatches 124;	Indels 2;	Gaps 2;		
QY	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLS	CMPPNSTYDYFLLPAGLSKNTS	NS	60		
Db	1	MMCQKFYVLLHWEFIYVIAALNLAYPISPWKFL	FCGPPNTTDDSFSPAGAPNNAS	AL	60		
QY	61	NGHYETA	VEPKFNSGTHFSNLSKTTTFHCCFRSEQDRNCSLCADN	IEGKTFVSTVNSLVF	120		
Db	61	KGASEA	IVEAKFNSSGIYVP	PELSKTVFHCCFCGNEQGNC	SALT	120	
QY	121	QQIDANWNI	QCWLKGLKLFICYVESLFKNLFRN	YNYKVHLLYL	VLPEVLEDSPLVPQKGS	180	
Db	121	RQLGVNWD	IECWMKGLTLFICHMEPLKPNPKNYDSKVHLLY	DLPEVIDDSPLPLKDS	180		
QY	181	FQVHCNCSVHECCECLVPVPTAKLNDTLMLCLKIT	SGGVIFQSPLMSVQPINMVKPDPP	240			
Db	181	FQTVQNC	SLRG-CECHVPVPRAKNL	YALLMYLEITSAGVSFQSP	PLMSLQPMLVVKPDPP	239	
QY	241	LGLHMEITDDGNLKISWSSP	PLVPFPPLQYQVKYSENSTTVIREADKIVS	SATSLLDVDSILP	300		
Db	240	LGLHMEVTDGNLKISWDSQ	TMAPFPLOQYQVYLENS-TIVREAAEIVS	SATSLLDVDSVLP	298		
QY	301	GSSYE	QVRGKRLDGP	GIWSDWSTPRVFTTQDVIYFP	PKILTSVGSNVSFHCYKKNKI	360	
Db	299	GSSYE	QVRSKRLDGG	SGVWSDWSSPQVFTTQDVVYFP	PKILTSVGSNASFHCYKKNQI	358	
QY	361	VPSKEI	VWMMNLA	EKIPOSQYDVVSDHVS	KVTFFENLNETKPRGKFTYDAVYCCNEHCHH	420	
Db	359	ISSKQI	VWMMNLA	EKIPEIQYSIVSDRVSKVTF	PSNLKATRPRGKFTYDAVYCCNEQACHH	418	
QY	421	RYAELY	VIDVNIINIS	CETDGYLT	KMTCRWSTSTFQSLAESTLQ	LRYHRSSLYCSDIPSIIH	480
Db	419	RYAELY	VIDVNIINIS	CETDGYLT	KMTCRWSPSTIQSLVSTVQLRYHRRS	LYCPDSPSIH	478
QY	481	PISEPK	DCYLQSDGFYECIFQPIFLLSGY	TMTIRINHSLSGLDSPPTCVLP	DSVVKPLPP	540	
Db	479	PTSEPK	NCVLQDGFYECV	FQPIFLLSGY	TMTIRINHSLSGLDSPPTCVLP	DSVVKPLPP	538
QY	541	SSVKA	EITINIGLLKISWEKVP	FVPENNLFQIRYGLSGKEVQWKMYE	VDAKSKSVSLPV	600	
Db	539	SNVKA	EITVNTGLLKVSWEKVP	FVPENNLFQIRYGLSGKEIQWK	THEVFDKSKSASLLV	598	
QY	601	PDLCA	VYAVQVRCKRLDGLGYWSN	WSNPAYTVVMDIKVPMRGPEFWRI	INGDTMKKEKNV	660	
Db	599	SDLCA	VYVQVRCRRLDGLGYWSN	WSSPAYTLVMDVKVPMRGPEFWRKMDG	VDVTKKERNV	658	
QY	661	TLLWK	PLMKNDLSVQRYVINHHTSCNGTWSE	DVGNHTKFTFLWTEQAHTVTVLAIN	SI	720	
Db	659	TLLWK	PLTKNDLSVRRYVVKHRTAHNGTWSE	DVGNRTNLTLFLWTEPAHTVTVLAVNS	L	718	
QY	721	GASVA	NFNLTFSWPM	SKVNIQVQSL	SAYPLNSSCVIVSWILSPSDYKLMYF	II	780
Db	719	GASLV	NFNLTFSWPM	SKVSAVESLSAYPLSSSCVILSWT	LSPPDDYSLLYLV	VIEWKILNED	778
QY	781	GEIKW	LRISSVKKYI	HDHFIPIEKYQFSLPIFM	EGVCKPKIINSFTQDDIEKHQSDA	840	
Db	779	DGMKW	LRIPSNVKKFYI	HDNFIPIEKYQFSLPIFM	EGVCKPKIINGFTKDAIDKQONDA	838	
QY	841	GLYVI	VPVIIS	SILLGLTLLISHQRMK	KLFWEDVPNPKNC	SWAQGLNFQKPF	900
Db	839	GLYVI	VPPIIIS	CVLLGLTLLISHQRMK	KLFWDDVPNPKNC	SWAQGLNFQKDI	898
RESULT 4							
S68439							
leptin receptor, splice form Ob-Rc - mouse							

Db 359 ISSKQIVWMRLAEKIPQISIVSDRVSKVTFSNLKATRPGRGKFTYDAVYCCNEQAACH 418

QY 421 RYAELYVIDVININISCETDGYLTGMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSII 480

Db 419 RYAELYVIDVININISCETDGYLTGMTCRWSTSTIQSLVGVSTQVLRVHRSSLYCPDPSII 478

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540

Db 479 PTSEPKNCVLQDGFYECVFOPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEVDYDAKSKSVSLPV 600

Db 539 SNVKAETITNTGLLKVSWEKPVFPENNLOFQIRYGLSGKEIQWKTHEVDFDAKSKSASLLV 598

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

Db 599 SDLCAVYVQVRCRRLDGLGYWSNWSNPAYTLVMDVVKVPMRGPEFWRKMDGDVTKKERNV 658

QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSESDVGNHTKFTFLWTEQAHTVTVLAINSI 720

Db 659 TLLWKPLTKNDSLCSVRRYVVKHRTAHNGTWSESDVGNRTNLTFLWTEPAHTVTVLAVNSL 718

QY 721 GASVANFNLTFSWPMKSVNIVQSLAYSPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780

Db 719 GASLVNFNLTFSWPMKSVSAVESLSAYPLSSCVILSWTLSPDDYSLLYLVIEWKILNED 778

QY 781 GEIKWLRISSVKYYIHDHFIPIEKYQFSLPIFMGVGKPKIINSFTQDDIEKHQSDA 840

Db 779 DGMKWLRIPIPSNVKKFYIHDNFIPYQFSLPVFMGVGKPKIINGFTKDAIDKQONDA 838

QY 841 GLYVIVPVIISILLGLTLLISHQRMKFLFWDVVPNPKNCSWAQLNFQK 891

Db 839 GLYVIVPIIISCVLLGLTLLISHQRMKFLFWDVVPNPKNCSWAQLNFQK 889

RESULT 6

S74225

leptin receptor, isoform Ob-Rf - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999

C:Accession: S74225

R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.

FEBS Lett. 392, 87-90, 1996

A:Title: A novel leptin receptor isoform in rat.

A:Reference number: S74225; MUID:96368027

A:Accession: S74225

A:Molecule type: mRNA

A:Residues: 1-895 <WAN>

A:Cross-references: EMBL:U53144; NID:g1395212; PIDN:AAB03088.1; PID:g1395213

A:Experimental source: strain Sprague-Dawley; tissue type brain

C:Genetics:

A:Gene: rOb-R

C:Keywords: appetite; transmembrane protein

F:840-860/Domain: transmembrane #status predicted <TMM>

Query Match 59.6%; Score 3729; DB 2; Length 895;

Best Local Similarity 76.5%; Pred. No. 2e-234;

Matches 682; Conservative 84; Mismatches 123; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFYIVITAFNLSPITPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60

Db 1 MTCQKFYVLLHWEFLYVITALNLAYPTSPWRFKLFCAPPSTTDDSLSPAGVPNNTSSL 60

QY 61 NGHYETAPEKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

Db 61 KGASEALVEAKFNSTGIYVSELSKTIHFCCFGNEQGNCSALTGNTGKTLASVVKPLVF 120

QY 121 QQIDANWNTQWLKGDCLKFICYVESLFPKNLFRNRYKVHLLYVLPVEYLEDSPVPQKGS 180

Db 121 RQLGVNWDIECWKMGDLTLFICHMEPLLNKPNFKNYDSKVHLLYDLPVEYDLDLPPLKDS 180

QY 181 FQMVHCNCSVHECCCLVPVPPTAKLNDTLLMCLKITSGGVIFQSPMSVQPINMWKPDPP 240

Db 181 FQTVQCNCVSRE-CECHVPVPRAKVNYALLMYLEITSAGVSFQSPLMSLQPMLVVVKPDPP 239

QY 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVYKYSNSTTVIREADKIVSATSLLDVDSILP 300

Db 240 LGLRMEVTDGNNLKISWSDSQTKAPFPLOQYKYLENS-TIVRAAEIIVSDTSLLDVDSVLP 298

QY 301 GSSYEVOVRGKRLLDGPINSDWSTPRVFTTQDVIYFPPPKILTSGSNVSPFHCYKKNKI 360

Db 299 GSSYEVOVRSKRLLDGSWSDSLPQLFTTQDVMYFPPPKILTSGSNASFPCCIYKKNQOT 358

QY 361 VPSKEIVWMNLAEKIPQSQDYVSDHVSKVTFFFNLNETKPRGKFTYDAVYCCNEHECHH 420

Db 359 ISSKQIVWMNLAEKIPETQYNTVSDHISKVTFNSNLKATRPGRGKFTYDAVYCCNEQCOQH 418

QY 421 RYAELYVIDVININISCETDGYLTGMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSII 480

Db 419 RYADLYVIDVININISCETDGYLTGMTCRWSPSTIQSLVGVSTQVLRVHRSSLYCPDNPSIR 478

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540

Db 479 PTSELKNCVLQDGLYECVSOPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEVDYDAKSKSVSLPV 600

Db 539 SNVKAETITNTGLLKVSWEKPVFPENNLOFQIRYGLNGKEIQWKTHEVDFDAKSKSASLPV 598

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

Db 599 SDLCAVYVQVRCRLDGLGYWSNWSNPAYTLVMDVVKVPMRGPEFWRIINGDTMKKERNV 658

QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSESDVGNHTKFTFLWTEQAHTVTVLAINSI 720

Db 659 TLLWKPLMKNDSLCSVRRYVVKHRTAHNGTWQDVGNTNLTFLSGESAHTVTVLDINSI 718

QY 721 GASVANFNLTFSWPMKSVNIVQSLAYSPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780

Db 719 GASLVNFNLTFSWPMKSVNGWQSLAYSPLSSCVILSWTLSPNDYSLLYLVIEWKNLNDD 778

QY 781 GEIKWLRISSVKYYIHDHFIPIEKYQFSLPIFMGVGKPKIINSFTQDDIEKHQSDA 840

Db 779 DGMKWLRIPIPSNVNKYYIHDNFIPYQFSLPVFMGVGKPKIINGFTKDDIAKQONDA 838

QY 841 GLYVIVPVIISILLGLTLLISHQRMKFLFWDVVPNPKNCSWAQLNFQK 891

Db 839 GLYVIVPIIISCVLLGLTLLISHQRMKFLFWDVVPNPKNCSWAQLNFQK 889

RESULT 7

S68441

leptin receptor, splice form Ob-Re - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000

C:Accession: S68441

R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;

Nature 379, 632-635, 1996

A:Title: Abnormal splicing of the leptin receptor in diabetic mice.

A:Reference number: S68437; MUID:96231997

A:Accession: S68441

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-805 <LEE>

A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493

A:Experimental source: splice form Re; tissue hypothalamus

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:

C:Genetics:

A:Gene: Ob-Re

C:Keywords: alternative splicing; appetite

Query Match 53.4%; Score 3340; DB 2; Length 805;

Best Local Similarity 76.2%; Pred. No. 3.5e-209;

QY 999 GEOGLINSSVTK-CFSSKNSP-----LKDSFSNSSWEIBAQAFFILSDQHPNIISPHLTF 1053
Db 770 PSVQVFSRSESTQPLLDSEERPEDQLVDSVDGGDEILPRQPYFKONCSQPE-ACPEISH 828
QY 1054 SEGLDELLKLEGN 1066
Db 829 FERSNQV--LSGN 839
RESULT 9
A36337
membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C;Accession: A36337
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A;Reference number: A36337; MUID:9108484
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <HIB>
A;Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C;Genetics:
A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>
Query Match 5.5%; Score 345.5; DB 2; Length 918;
Best Local Similarity 19.8%; Pred. No. 2.6e-14;
Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;
QY 337 PPKILTSGNSVSHCIYKK---ENKIVPSKEIVWMMNLAEKIPQSQYDVVSDHVSKVTF 393
Db 33 PESPVQLHSNFTAVCVLKEKCMDFHVNANYIVWKTN-HTIPKEQYTIINRTASSVTF 91
QY 394 FNLNETPRGKFTYDAVYCCNEHCHRYAELIVDV-----NINISC-ETDGYLTK 444
Db 92 TDI-----ASLNQLTCNLTFTGQLEQNQVYGITIISGLPPEKPKNLSCIVNEG--KK 141
QY 445 MTCRWSTSTIQSLAESTLQRYHRSSLYCSDIPSIIHPISEPKDCYLQSDGFYECI--FQP 502
Db 142 MRCEWDGG-----RETHLETNFTLKSEWAT-----HKFA--DCKAKRDTPTCTVDYST 188
QY 503 IFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPSSVKAETIN-----IGLLKISW 558
Db 189 VYFVN-IEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNL-----VINSEELSSILKLTW 244
QY 559 EKP-----VFPENNLOFQIRYGLSGKEVQWKMYEVDKSKSVLPVPDL--CAVYAVQV 611
Db 245 TNPSIKSVILKYNIQYRTKDAST-----WSQIPPEDTASTRSSFTVQDLKPFTEYVFRI 299
QY 612 RCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLWLKPLMKND 671
Db 300 RCMKEDGKYWSWDWSEASGITTEDR-PSKAPSFYKIDPSHTQGYRTVQLVWKTLPPE 358
QY 672 SLCSVQRYVINHHTSCNGTWSEVDGNH-----TKFTFLWTEQAHTVTVLAINSIGASVANE 727
Db 359 ANGKILDYEV-----LTRWKSILQNYTVNATKLTNLTNDRYLATLTVRNLVGKSDAAV 413
QY 728 NLFTSWPMKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMFYFIEWKNLNEDGE--IKW 785
Db 414 LTIPACDFQATHPVMDLKAFP-KDNMLWVETWTPRESVK--KYILEWCVLSDKAPCIDW 470
QY 786 LRISSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKII----- 825
Db 471 QQEDGVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPVTRTKV 530

QY 826 -----NSFTQDDIEKHQSDAGLY- 843
Db 531 GKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTETLSSLTSDT-LYM 589
QY 844 -----VIVPVISSSI-LLGLTLLISHQR--MKK 869
Db 590 VRMAAYTDEGGKDGPEFTFTTPKFAQGEIAIVVPCVLAFLTLTLLGVLCFNKRDLIKK 649
QY 870 LFWEDVPNPKNCSWAQGLNFQKPFTEHFLFIKHTASVTCGPIILLEPETISEDISVDTSWK 929
Db 650 HIWPNVPDPSKSHIAQWSPHTPP-----RH-----NFN 677
QY 930 NKDENMPTTVVSLSTTDLEKGSVCISDQFNSVNFSEAEGETVYEDESQRQPF---VKY 986
Db 678 SKDQM-----YSDGNFTDVSVEIEAND---KKPFPEDLKS 710
QY 987 ATLISNKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSS 1028
Db 711 LDLFKKEKINTEGSHSGIGGSS---CMSSSRPSISSSDENES 749
RESULT 10
A44257
interleukin-6 signal transducing molecule gp130 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C;Accession: A44257
R;Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A;Title: Molecular cloning and characterization of the rat liver IL-6 signal transduc
A;Reference number: A44257; MUID:93052397
A;Accession: A44257
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-918 <WAN>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:118488)
C;Superfamily: cytokine receptor homology
C;Keywords: transmembrane protein
F;134-315/Domain: cytokine receptor homology <CRS>
Query Match 5.4%; Score 339.5; DB 2; Length 918;
Best Local Similarity 20.8%; Pred. No. 6.3e-14;
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;
QY 327 VFTTQDVI-----YFPFKILTSGNSVSHCIYKKENKIVPSKE---IWWWNNLAE 374
Db 14 IFLTTEIGQLVEPCGYIYEPFPVQSGSNFTATCVLKEKCLQVYSVNATYIVWKTNHV- 72
QY 375 KIPQSQYDVVSDHVSKVTFEFLNETPRGKFTYDAVY-----CCNEHCHRYAELYVI- 428
Db 73 AVPKEQVTVINRTASSVTF-----TDVVFQNVQLTCNLSLFGQIEQNVIYGIT 119
QY 429 -----DVNINISC-ETDGYLTKMTCRWSTSTIQSLAESTLQRYHRSSLYCSDIPSIIH 480
Db 120 ILSGYPPDIPTNLSCIVNEG--KNMLCQ-----LDPGRETYLETNLTLKSEWATE----- 167
QY 481 PISEPKDCYLQSDGFYECI--FOPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPL 538
Db 168 ---KFPDCRTK-HGTSSCMMGYTIPIFVN-IEVWVEAENALGNVSSEPIFDPVDKVKPS 222
QY 539 PPSSVKAETINI-GLLKISW-----EKPVEPENNLOFQIRYGLSGKEVQWKMYEVDK 592
Db 223 PPHNLSVTNSEELSSILKLAWNNSGLDSILRLKSDIQYRTKDAST-----WIOVPLEDTV 277
QY 593 SKSVSLPVPDL--CAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIIN 650
Db 278 SPRTSFTVQDLKPFTEYVFRIRSIKENGKGYWSWSEASGITTEDR-PSKAPSFYKVN 336
QY 651 GDTMKKEKNVTLWLKPLMKNDSLCSVQRY--VINHHTSCNGTWSEVDGNHTKFTFLWTEQ 708
Db 337 ANHPQEYRSARLIWKTLP LSEANGKILDYEVVLTQSKSVSQTYTV---NGTELIVNLTN 393

QY 195 -----ECLVPVPTAKLNDTLLMCLKITSGVIFQSPLMSVQPINMVKPDPLGLHMEIT- 248
Db 90 CYQLEKTSIKIPALSHGDYEITINSLHDFGSSTSKFTLNEQNVSLI-PDTPEILNLSADF 148
QY 249 DDGNLKISWSSPPLVPFPLQYQVKYSENSTVIR---EADKIVSATSL- 294
Db 149 STSTLYLKWDRGSV-FPHRSNVIV---EIKVLRKESMELVKLVHTHTLNGKDTLHHWS 204
QY 295 --VDSILPGSSYEQVR---GKRLDGPGLIWSDWSTPRVFT---TQDVLYFPKILTSVG 345
Db 205 WASDMPLECAIHFEIRCIYIDNLHFGLEEWSWSPVKNISWIPDSQTKVPFQDKVILVG 264
QY 346 SNVSFHCIVKKNKIVPSKEIVVMMNLAEKIPQSQYDVV---SDHYSKVTFNLTNETKPR 402
Db 265 SDITFCV-----SQEKV-----LSALIGHTNCPLIHLHDGENVA-IKIRNISVSASS 310
QY 403 GKFTYDAVYCCNEHECHHRYAEALYVIDVNNINISCETDGYLTMTCRWSTSTIQSLA---E 459
Db 311 GT---NVVFTTEDNIFGTIVIFAGYPPDTPQOLNCETHD-LKEIICSWNPGRVTAIVGPR 366
QY 460 STLQRLYHRSSLYCSDIPSIHPISSEPKDCVQLQSDGFYECIFQPIFLLSGYTMWIRINHS 519
Db 367 TSYTLVESFSKYYVRLKRAEAPTNE-----YQLLFQMLPQBEIYNFTLNAHNPL 416
QY 520 GSLDSPPTCVLPDSVVVKPLPPSSVKAETINIGLLKISWEKP-----VFPE 566
Db 417 GRSQSTILVNTTEKVY-PHTPTSFVKV-DINSTAVKLSWHLPGNFKINFLCEIEIKKSN 474
QY 567 NLQFOIRYGLSGKEVQWKMYEYDASKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWS 626
Db 475 SVQEQRNVTIKGE-----NSSYLVALDKLNPYTLTYTFRIRCS-TETFWKWSKWS 523
QY 627 NPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNDLSQVQRYVINHHTS 686
Db 524 NKKQHLTTEAS-PSKGPDTWREWS-----GKNLIYWKPLPINEA-----NGKILSYNVS 574
QY 687 CNG-----TWSEEDVGNHTKFTFLWTEQAHVTVTVLAINSIGASVANFNLTFSWPMKVNIV 741
Db 575 CSSDEETQSLSEIPDPQHKAEIRLDKNDYIISVAKNSVSGSSPPSKIASMEIPNDCLKIE 634
QY 742 QLSAYPLNSSCVIVSWILSPS---DYKLMYFIIWKVKN-LNEDGEIKWLRI-SSSVKKY 795
Db 635 QVVGW---GKGLLTWHYDPNMTCDY-----VIKWCNSSRSEPCLMWRKVPNSSTETV 685
QY 796 YIHDHFIPKIEKYQFSLPIFMEG-----VG-----KPKIINSETQDD----- 832
Db 686 IESDEFRPGIRNFYLYGCRNQGYQLLRSMYIEELAPIVAPNFTVETSADSILVKWE 745
QY 833 -----IEKHQSD----- 839
Db 746 DIPVEELRGFLRGYLYFYFGKGERDTSKMRVLESGRSDIKVKNITDISOKTLRIADLOKGT 805
QY 840 -----AGLYVI-----VPVLISSSILLGLTLLISHQR--M 867
Db 806 SYHLVLRAYTDGGVGPEKSMYVVTKENSVGLIAILIPVAVAVIVGVVTSILCYRKREWI 865
QY 868 KKLFWEDVNPKNCSWAQGLNFQK-----PETFEHLFTKHTASVTCGPPL 912
Db 866 KETFYPDIPNENC---KALQFQKSVCEGSSALKTLEMNPTPNNVELETRSAF--PKI 920
QY 913 LEPETISEDISVDTSWKNKDEMMPTTVVLSLSTDLKGSVC---ISDPNSVNFSEAE 969
Db 921 EDTEIIS---PVAERPEDRSDAEPENHVW-----SYCPPIIEEIPNPAADEAG 968
QY 970 T-EVTYED-ESQRPVVKYATLISNSKPSERGEQGL-----INSSVTKCF- 1014
Db 969 TAQVIYIDVQSMYQP-----QAKPEEQENDPVGGAGYKPKQMHLPINSTVEDIAAE 1019
QY 1015 ---SKNSPLKDSFNSSSWEIEAQAFILSDOHPNIIISP 1049
Db 1020 EDLDKTAGYRPOANVTW-----NLVSP 1042

RESULT 13
C38252
N:Contains: granulocyte colony-stimulating factor receptor precursor, long form - human
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C:Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A:Note: clones pHG11 and pHG5
A:Accession: A38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FU2>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A:Note: clone pHQ3
R:Rarsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <LAR>
A:Cross-references: GB:X55721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A:Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A:Molecule type: DNA
A:Residues: 855-863 <SET>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A:Experimental source: granulocyte
A:Note: sequence extracted from NCHI backbone (NCBIN:71484, NCBIP:71485)
R:Hanlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
A:Accession: S68332
A:Molecule type: protein
A:Residues: 234-269 <HAN>
C:Genetics:
A:Gene: GDB:CSF3R
A:Cross-references: GDB:126430; OMIM:138971
A:Map position: lp35-lp34.3
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F;25-680,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F;25-627/Domain: extracellular #status predicted <EXT>
F;628-653/Domain: transmembrane #status predicted <TM>
F;654-863/Domain: intracellular #status predicted <INT>
F;93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 4.6%; Score 288.5; DB 2; Length 863;
Best Local Similarity 20.0%; Pred. No. 1.2e-10;
Matches 156; Conservative 125; Mismatches 280; Indels 219; Gaps 38;

QY 341 LTSVGSNVSFHCIVKKE-NKIVPSKEIVVMMNLAEKIPQSQYDVSD--HVSKVTFN 397
Db 35 IVHLGDPITASCIIKQNCSHLDPEPQILWRLG-AELQPGGRQORLSDGTQESI 93
QY 398 ETKPRGKFTYDAVYCCNEHECHHRYAEALYVID-----VNINISCETDGYLT 446

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Db 94 HTQ-----AFLSC-----CLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLI 141
QY 447 CRWSTSTIQSLAES-TLQLRYHRSSLYCSDIPSIHPSEPKCYLQSDGFYECI----- 499
Db 142 CQWEPGPETHLPTSTFLKFSKRG-----NCQTQGDSILDCVPRKDGQS 184
QY 500 -----FQIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP-----SSVKAET 548
Db 185 HCCIPRKHLLLYQNMGIVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEA-AP 243
QY 549 INIGLLKISWEKPVFP--ENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPVP----- 601
Db 244 PQAGCLQLCWE-PWQPGHLHINQKCELRHKPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCAV-----YAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGP-----EFWRILN 650
Db 292 YELCGLLPATAYTLQIRCIWPLPGHWSDFS-PS---LELRTERAPTVRDLTWWR--- 343
QY 651 GDTMKKEKNVTLLWKPLMKNDLSVQRYVINHHTS-----CNGTWSDEVGNHTKF 701
Db 344 -QRQLDPRTVQLFWKVPVLEEDSGRIQYVVSWRPSCGAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQAHTVTVLAINSGASVANFNLTFSWPMKSKVNIQVSLASAYPLNSSCVIVSWILS 761
Db 396 TFLPSEAQAEVALVAYNSAGTSRPT-PVVFES--ESRGPALTRLHAMARDPHSLWVGW--E 450
QY 762 PSDYKLMYFIIEW-----KNLNEDGEIKW-LRISSSVKKYYIHDHFIPIEKYQPSLYP 813
Db 451 PPNWPQGYVIEWGLGPPSASNSNK-----TWMEQNGRATGFLLENIRPFQLYEIVTP 506
QY 814 IFMEGVGKPKIINSETQDDIEKHQSDAGL-----YVIVPVISSSILLGLTLLI 862
Db 507 LYQDTMGPSQHVYAYSQEMAPSHAPELHLKHIGKTWAQLEWVPEPELGKSPPLTHYT--- 563
QY 938 --TVVSL-----STTDLEKGSV--CISDQFNSVNFSEAEGETEYDEESQRQP 982
Db 674 VPTIMEELPGPRQGWLGOTSEMSRALTPHPCVQDAFQLPGLGTPPTITKLTVLEDEKKP 733

RESULT 14
JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C;Accession: JH0329; S21608
R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Son
J. Exp. Med. 172, 1559-1570, 1990
A;Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A;Reference number: JH0329; MUID:91079757
A;Accession: JH0329
A;Molecule type: mRNA
A;Residues: 1-783 <LAR>
A;Cross-references: GB:X55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A;Experimental source: placenta
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-783/Product: granulocyte.colony-stimulating factor receptor D7 #status predicted <M
F;25-627/Domain: extracellular #status predicted <EXT>
F;628-653/Domain: transmembrane #status predicted <TRA>
F;654-783/Domain: intracellular #status predicted <INT>
F;93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict
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Query Match 4.5% Score 284; DB 2; Length 783;

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Best Local Similarity 20.3%; Pred. No. 2e-10;
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QY 341 LTVSGNSVSHFHCYKKE-NKIVPSKEIVWMMNLAEKIPQSQDYDVVSD--HVSKVTFEFLN 397
Db 35 IVHLGDPITASCIKQNCCHLDPEQILWRLG-AELQPGGRQORLSDGTQESIITLPHLN 93
QY 398 ETKPRGKFTYDAVYCCNEHCHRYAELVID-----VNINISCETDGYLTGMT 446
Db 94 HTQ-----AFLSC-----CLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLI 141
QY 447 CRWSTSTIQSLAES-TLQLRYHRSSLYCSDIPSIHPSEPKCYLQSDGFYECI----- 499
Db 142 CQWEPGPETHLPTSTFLKFSKRG-----NCQTQGDSILDCVPRKDGQS 184
QY 500 -----FQIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP-----SSVKAET 548
Db 185 HCCIPRKHLLLYQNMGIVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEA-AP 243
QY 549 INIGLLKISWEKPVFP--ENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPVP----- 601
Db 244 PQAGCLQLCWE-PWQPGHLHINQKCELRHKPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCAV-----YAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGP-----EFWRILN 650
Db 292 YELCGLLPATAYTLQIRCIWPLPGHWSDFS-PS---LELRTERAPTVRDLTWWR--- 343
QY 651 GDTMKKEKNVTLLWKPLMKNDLSVQRYVINHHTS-----CNGTWSDEVGNHTKF 701
Db 344 -QRQLDPRTVQLFWKVPVLEEDSGRIQYVVSWRPSCGAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQAHTVTVLAINSGASVANFNLTFSWPMKSKVNIQVSLASAYPLNSSCVIVSWILS 761
Db 396 TFLPSEAQAEVALVAYNSAGTSRPT-PVVFES--ESRGPALTRLHAMARDPHSLWVGW--E 450
QY 762 PSDYKLMYFIIEW-----KNLNEDGEIKW-LRISSSVKKYYIHDHFIPIEKYQPSLYP 813
Db 451 PPNWPQGYVIEWGLGPPSASNSNK-----TWMEQNGRATGFLLENIRPFQLYEIVTP 506
QY 814 IFMEGVGKPKIINSETQDDIEKHQSDAGL-----YVIVPVISSSILLGLTLLI 862
Db 507 LYQDTMGPSQHVYAYSQEMAPSHAPELHLKHIGKTWAQLEWVPEPELGKSPPLTHYT--- 563
QY 863 SHQRMKKLFWEDVPNPKNCWAQGLNFQ-----KPTFEHLFIK-----HTASVT 907
Db 564 -----IFW---TNAQNSFSAILNASSRGFVLHGLEPASLYHIHLMAASQAGATNSTV 613
QY 908 CGPLLLEPETISEDISV-----DTSW-----KNKDEMMPTTVVSLSTTDLE 949
Db 614 LTLMTLTPEGSELHIILGLFGLLLLTCLCGTAWLCCSPNRKNPLWPSVPDPHAHSSLSGSW 673
QY 950 KGSVCISDQFNSVNFSEAEGETEYDEESQRQP 982
Db 674 VPTIMEEDAFQLPGLGTPPTITKLTVLEDEKKP 706

RESULT 15
JX0312
differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor -
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C;Accession: JX0312; JC2181; S38942
R;Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
J. Biochem. 115, 557-562, 1994
A;Title: Three different cDNAs encoding mouse D-factor/LIF receptor.
A;Reference number: JX0312; MUID:94334302
A;Accession: JX0312
A;Molecule type: mRNA
A;Residues: 1-1092 <TOM>
A;Cross-references: DDBJ:D26177; NID:g473718; PIDN:BAA05165.1; PID:dl005707; PID:g825
A;Accession: JC2181
A;Molecule type: mRNA
A;Residues: 1-717,'EA' <TOM1>
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A;Cross-references: DBJ:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494
A;Experimental source: liver
R;Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
FEBS Lett. 334, 193-197, 1993
A;Title: Pregnancy associated increase in mRNA for soluble D-factor/LIF receptor in mouse
A;Reference number: S38942; MUID:94039833
A;Accession: S38942
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-717,'EA' <TOM2>
A;Cross-references: GB:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494
C;Keywords: differentiation; receptor; transmembrane protein
F;1-43/Domain: signal sequence #status predicted <SIG>
F;44-1092/Product: differentiation-stimulating factor/leukemia inhibitory factor receptor
F;828-854/Domain: transmembrane #status predicted <TMM>

Query Match 4.5%; Score 281.5; DB 2; Length 1092;
Best Local Similarity 18.8%; Pred. No. 4.9e-10;
Matches 217; Conservative 177; Mismatches 392; Indels 371; Gaps 57;

QY	178	KGSGQVHVCNCSVHECCCLVPVP-----TAK---LNDTLLMC--LKITSGGVIFQSP-	225
Db	45	KRGVQDLKCTNNMRVWDCTWPAPLGVSPGTVKDICKDRFHSCHPLETTNNKIPALSPG	104
QY	226	-----LMSVQPINMVKPDPPPLGLHMEITDD---GNLKISWSS--PPLVPF	265
Db	105	DHEVTINYLNGFQSKFTLNEKDVSLIPETPEI---LDLSADFTSSLLKWNDRGSALPH	161
QY	266	P--LQYQVKYSENSTVIREADKIVSATSLL-----VDSILPGSSYEYVQVRGK	311
Db	162	PSNATWEIKVLQNPRT---EPVALVLLNTMLSGDKTQVQHNWNTSDLPLOCATHSVSIRW-	217
QY	312	RLDGPGI-----WSDWSTPRVFT---TQDVIYPPPKILTSGVNSVFHCIIYKKNKIVPS	363
Db	218	HIDSPHFSYKKEWSDWSPLKNISWIRNTETNVFPQDKVVLGASNMTICC-----MSPT	270
QY	364	KEIVWMW-NLAEKIPQSQYDVVSDHVSKVTFEFLNETKPRGK---FTYDAVYCCNEHEC	418
Db	271	KVLSGQIGNTLRLPLIHLGYQTVAIHI-----LNIPVSENSGTNIIFITDDDV-----	317
QY	419	HHRYAEL---YVIDVNINISCETDGYLTMTKTCRWSTSTIQSL-----AESIL-----	462
Db	318	---YGTVVFAGYPPDPQKLSCEHD-LKEIICSWNPGRITGLVGRNTEYTLFESISGK	373
QY	463	QLRYHR-----SSLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINH	517
Db	374	SAVFHRIEGLTNETYRLGV-QMHPGQEIHN-----FTLTG-----RN	409
QY	518	SLGSLDSPPTCVLPDSVVKPLPPSSVKAIEITINIGLLKISWEKP-VFPENNLFQIRYGL	576
Db	410	PLGQAQSAVINVTERVA-PHDPTSLKVK-DINSTVVTFSWYLPNGFTKINLLCQIEICK	467
QY	577	SGKEVQWKMEYVDKSKSVSLPVPDL--CAVYAVQVRCKRLDGLGYWSNWSNPAYTVVM	634
Db	468	ANSKKEVRNATIRGAEDSTYHVAVDKLNPTYATYTPRVRCSS-KTFWKWSRWSDEKRHLTT	526
QY	635	DIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSED	694
Db	527	E-ATPSKGPDTWREWSSD---GKNLIVYWKPLPINEA---NGKILSYNVSCS-----	571
QY	695	VGNHTKFTFLWTEQAH-----TVTVLAINSIGASVANFNLTFSWPMKVNIVQS	743
Db	572	LNEETQSVLEIFDPQHRABEIQLSKNDYIISVVARNSAGSSPPSKIASMEIPNDITVEQA	631
QY	744	LSAYPLNSSCVIVSWILSPS---DYKLMYFIIENKN--LNEDGEIKWLRI-SSSVKKYYI	797
Db	632	VGL-----GNRIFLTWRHDPNMTCDY-----VIKWCNSSRSEPCLLDWRKVPSNSTETVIE	682
QY	798	HDHFIPIEKYQFSLYPIFMEG-----VG-----KPKIINSFTQDD-----	832
Db	683	SDQFQPGVRYNFYLYGCTNQGYQLLRISIGYVEELAPIVAPNETVETSDSILVKWDDI	742

QY	833	-----IEKHQSDAGL-----	842
Db	743	PVEELRGFLRGYLFYQKGERDTPKTRSLPHHSIDIKLKNITDISQKTLRIADLQKTSY	802
QY	843	-----YVIVPVISSSILLGLTLLISHQR--MKK	869
Db	803	HLVLRAYTHGGLGPEKSMFVVTKENSGLIIAILIPVAVAVIVCVVTSILCYRKREWIKE	862
QY	870	LFWEDVPNPKNCNWAQGLNFQKPFETFEHLFIKHTASVTCGPLLLLEPETISEDISVDTSWK	929
Db	863	TFYPDIPNPENC---KALQFQKSVCEGSNALKTLEMNPTP-----NNVEVLESRS	910
QY	930	NKDEMMPTTVVSLSTDTLEKGSV-----CISDQFNSVNFSEAE-TEVTYE	975
Db	911	IVPKIEDTEIISPVAERPERSEVDPENHVVSVCYCPPIIEEITNPAADDEVGGASQVVI	970
QY	976	D-ESQRPVFKYATLISNPKPSETGEEQGLINSSVTKCFSSKN SPLKDSFSNSSWEIEAQ	1034
Db	971	DVQSMYQPAK-----AEEEQDV-----DPV-----	991
QY	1035	AFFILSDQHPNI---ISPHTFSEGLDELLKLEGNFPEENNDKKSIYYLGVTSIKKRESG	1091
Db	992	--VVAGYKPMRLPISPAVEDTAAEDEEGKTAGYRPOQANVTWNL---VSPDSPRS--	1042
QY	1092	VLLTDKSRVSCPPFPAPC	1108
Db	1043	---TDSNNEVVSFGSPC	1056

Search completed: August 15, 2002, 16:25:01
Job time: 301 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:18:50 ; Search time 101.13 Seconds
(without alignments)
1279.551 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEFIYVIT.....QTCSTQTHKIMENKMCCLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6254	100.0	1165	AAW24051	Human WSX receptor
2	6254	100.0	1165	AAE12609	Human Ob receptor
3	6254	100.0	1220	AAW34500	Obesity receptor D
4	6250	99.9	1165	AAE12551	Human Ob receptor
5	6246	99.9	1165	AA113474	Peptide Seq ID No:
6	6240	99.8	1165	AAW19116	Human Ob receptor.
7	5809	92.9	1221	AAW62544	Human ob-receptor
8	4831.5	77.3	970	AAW34499	Obesity receptor C
9	4826	77.2	896	AAW24052	Human WSX receptor
10	4826	77.2	923	AAW24053	Human WSX receptor
11	4826	77.2	972	AAW34497	Obesity receptor A

12	4826	77.2	999	18	AAW34498	Obesity receptor B
13	4819.5	77.1	958	18	AAW38214	Human OB-R variant
14	4819.5	77.1	958	18	AAW31911	Human OB-R leptin
15	4819.5	77.1	958	18	AAW19535	Human OB-R leptin
16	4819.5	77.1	958	18	AAW22773	Human haematopoiet
17	4816.5	77.0	960	17	AAW88910	Haematopoietin rec
18	4814	77.0	896	18	AAW50003	Human OB-R variant
19	4814	77.0	904	18	AAW50002	Human OB-R variant
20	4813	77.0	908	17	AAW88911	Haematopoietin rec
21	4811	76.9	898	17	AAW88912	Haematopoietin rec
22	4799	76.7	908	18	AAW19536	Variant form of hu
23	4785	76.5	896	18	AAW14841	Human haematopoietin
24	4784.5	76.5	1162	18	AAW34257	Rat wild-type ob r
25	4784.5	76.5	1162	18	AAW23398	Rat ob receptor (w
26	4778.5	76.4	1162	18	AAW23399	Rat ob receptor (f
27	4770.5	76.3	1162	18	AAW19115	Murine long form O
28	4770.5	76.3	1162	22	AAE12615	Murine long form O
29	4766.5	76.2	1162	20	AA113473	Peptide Seq ID No:
30	4574	73.1	883	19	AAW62543	Human ob-receptor
31	4554	72.8	839	18	AAW34502	Obesity receptor p
32	4421	70.7	815	20	AAW05701	Human OB receptor
33	4337	69.3	804	18	AAW34501	Obesity receptor p
34	4214.5	67.4	1015	18	AAW34259	Rat ob receptor is
35	3793	60.6	900	18	AAW22105	Murine leptin rece
36	3787	60.6	892	18	AAW34260	Rat ob receptor is
37	3787	60.6	894	18	AAW37337	Ob protein recepto
38	3787	60.6	895	18	AAW34258	Rat ob receptor is
39	3785	60.5	894	18	AAW24064	Murine WSX recepto
40	3785	60.5	894	18	AAW19114	Murine short form
41	3785	60.5	894	22	AAE12608	Murine short form
42	3781	60.5	894	18	AAW37338	Ob protein recepto
43	3479	55.6	842	18	AAW22102	Murine leptin rece
44	3340	53.4	805	18	AAW22106	Murine leptin rece
45	3143	50.3	783	18	AAW24054	Murine WSX recepto

ALIGNMENTS

RESULT 1
AAW24051
ID AAW24051 standard; Protein; 1165 AA.
XX
AC AAW24051;
XX
DT 17-MAR-1998 (first entry)
XX
DE Human WSX receptor variant 13.2.
XX
KW Human; WSX receptor; variant 13.2; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.
XX
OS Homo sapiens.
XX
PN WO9725425-A1.
XX
PD 17-JUL-1997.
XX
PF 07-JAN-1997; 97WO-US00325.
XX
PR 20-JUN-1996; 96US-0667197.
PR 08-JAN-1996; 96US-0585005.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX

DR WPI; 1997-372864/34.
DR N-PSDB; AAT85575.
XX
PT WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
XX
PS Claim 2; Pages 81-85; 219pp; English.
PS
CC The present sequence is the human WSX receptor variant 13.2,
CC which can be used to identify and purify ligands and activators.
CC An anti-WSX receptor antibody can be used as an agonist to activate
CC the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. WSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
XX
SQ Sequence 1165 AA;

Query Match 100.0%; Score 6254; DB 18; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEITYVITAFNLSYPTTPWRKLSKMPNSTYDYFLPAGLSKNTSNS 60
|||||
DB 1 micqkfcvllhweifyvitafnlsypttpwrklskmpnstydyflpagskntsns 60
|||||

QY 61 NGHYETAPEKFNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
|||||
DB 61 nghyetavepkfnssgthfsnlskttfhccfrseqdrncslcadniegkftfstvnslvf 120
|||||

QY 121 QQIDANWNIOCWLGDLKLFICYVESLFKNLFNRYNYKVHLLYVLPEVLEDSPLVPQKGS 180
|||||
DB 121 qqldanwniqcwlqgdllkfcyveslfknlfnrynykvhllylvpeviedsplvpqkgs 180
|||||

QY 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMVSQPINMVKPDPP 240
|||||
DB 181 fqmvhcnscsvheccglvpvptaklndtlmlclkitsggvifqspmlsvqpinmvpkdpdp 240
|||||

QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQVQYKSENSTTVIREADKIVSATSLLDVDSILP 300
|||||
DB 241 lglhmeitddgnlkswsppplvpfploqyqvkysensttvireadkivsatslldvdsilp 300
|||||

QY 301 GSSYEVQVRGKRLDGPGIWSDNSTPRVFTTQDVYFPPPKILTSVGSNVSPHCYKKNKI 360
|||||
DB 301 gssyevqvrgrldgpgiwsdnstprvfttgdviyfpkpiltsvgsnvsfhciykkkenki 360
|||||

QY 361 VPSKEIVWMNLAEKIPQSQDYVSDHVSQVTKVFPFNLNETKPRGKFTYDAVYCCNEHECHH 420
|||||
DB 361 vpskeivwmnlaekipqsqdyvsvdhvskvtfvfnlnetkprgkftydavyccnehechh 420
|||||

QY 421 RYAELYVIDVNIINISCTDGYLTMTKTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480
|||||
DB 421 ryaelyvldvniiniscetdgyltkmtcrwststiqslaestlqlryhrsslycsdipsih 480
|||||

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
|||||
DB 481 pisepkdcylqsdgfyecifqipifllsgytmwirinhsldspptcvlpdsvvkplpp 540
|||||

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
|||||

Db 541 ssvkaeitinigllkiswekpvfpennlqfiryglsgkevqwkmyevydaksksvslpv 600

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
|||||

Db 601 pdlcavayavqrckrldglgywsnwsnpaytvvmdikvpmrgpgefwrriingdtmkkeknv 660
|||||

QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHHTKFTFLWTEQAHTVTVLAINSI 720
|||||

Db 661 tllwkplmkndslcsvqryvinhhtscngtwsedvgnhhtkftflwtegahtvtvlainsi 720
|||||

QY 721 GASVANENLTFESWPMKVNIVQSLAYSAPLNSSCSVIVSWILSPSDYKLMFYFIEWKNLNED 780
|||||

Db 721 gasvanfntfswpmkvnivqslaysaplnsscvivswilspdyklymfiewknlnd 780
|||||

QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLPIFMEGVGPKKIINSFTQDDIEKHQSDA 840
|||||

Db 781 geikwlrisssvkkyyihdhfipiekyqfslpifmegvgkpkilnsftqddiekhqsd 840
|||||

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWSAQGLNFQKPETFEHLFI 900
|||||

Db 841 glyvivpviissillgltllishqrmkklfwedvnpnkncswaqqglnfqkpetfehlfi 900
|||||

QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMMPPTVWSLLSTTDLEKGSVCISDQFN 960
|||||

Db 901 khtasvtcgpllepetisedisvdtswknkdemmpptvwsllstdlekgsvcisdqfn 960
|||||

QY 961 SVNFSAEAGTEVYDESRQPFVKYATLISNPKSETGEEQGLINSSVTKCFSSKNSPL 1020
|||||

Db 961 svnfsaeagtevydesrqpfvkayatlisnkpsetgeeqglinssvtkcfssknspl 1020
|||||

QY 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNKKSIYYL 1080
|||||

Db 1021 kdsfnsnweweieaqafilsdqhpniisphltfsegldeallklegnfpeenndkksiyyl 1080
|||||

QY 1081 GVTSIKKRESGVLLTQKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
|||||

Db 1081 gvtsikkrsgvlltdksrvscfpapclftdirvlqdschfvenninlgtsskktffas 1140
|||||

QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
|||||

Db 1141 ympqfqtctstqthkimenkmdltv 1165
|||||

RESULT 2
AAE12609
ID AAE12609 standard; Protein; 1165 AA.
XX
AC AAE12609;
XX
DT 03-JAN-2002 (first entry)
XX
DE Human Ob receptor (ObR) protein.
XX
KW Human; obese receptor; ObR; anorectic; anabolic; body weight disorder;
KW therapy; obesity; cachexia; anorexia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide
FT Protein 21..1165
FT /label= Human_mature_ObR_protein
FT Domain 21..839
FT /label= Extracellular_domain
FT Modified-site 23..25
FT /note= "Asn is N-glycosylated"
FT Modified-site 41..43
FT /note= "Asn is N-glycosylated"
FT Modified-site 56..58
FT /note= "Asn is N-glycosylated"
FT Modified-site 59..61
FT /note= "Asn is N-glycosylated"

FT Modified-site 73..75 /note= "Asn is N-glycosylated"

FT Modified-site 98..100 /note= "Asn is N-glycosylated"

FT Modified-site 187..189 /note= "Asn is N-glycosylated"

FT Modified-site 206..208 /note= "Asn is N-glycosylated"

FT Modified-site 276..278 /note= "Asn is N-glycosylated"

FT Modified-site 347..349 /note= "Asn is N-glycosylated"

FT Modified-site 319..323 /note= "Asn is N-glycosylated"

FT Region 397..399 /note= "Conserved motif of cytokine I receptor family"

FT Modified-site 433..435 /note= "Asn is N-glycosylated"

FT Modified-site 516..518 /note= "Asn is N-glycosylated"

FT Modified-site 622..626 /note= "Asn is N-glycosylated"

FT Region 624..626 /note= "Conserved motif of cytokine I receptor family"

FT Modified-site 659..661 /note= "Asn is N-glycosylated"

FT Modified-site 670..672 /note= "Asn is N-glycosylated"

FT Modified-site 688..690 /note= "Asn is N-glycosylated"

FT Modified-site 697..699 /note= "Asn is N-glycosylated"

FT Modified-site 728..730 /note= "Asn is N-glycosylated"

FT Modified-site 750..752 /note= "Asn is N-glycosylated"

FT Domain 840..862 /label= Transmembrane_domain

FT Domain 863..1165 /label= Cytoplasmic_domain

PN US6287782-B1.

PD 11-SEP-2001.

XX 29-APR-1998; 98US-0069781.

PR 27-NOV-1995; 95US-0562663.

PR 04-DEC-1995; 95US-0566622.

PR 08-DEC-1995; 95US-0569485.

PR 11-DEC-1995; 95US-0570142.

PR 28-DEC-1995; 95US-0583153.

PR 22-JAN-1996; 96US-0599455.

PR 26-APR-1996; 96US-0638524.

PR 03-SEP-1996; 96US-0708123.

PR 28-MAY-1997; 97US-0864564.

XX (MILL-) MILLENNIUM PHARM INC.

PA Tartaglia LA, Tepper RI, Culpepper JA, White DW;

PI WPI; 2001-624489/72.

XX N-PSDB; AAD20509.

DR Identifying compounds for treating body weight disorder, e.g. obesity,

PT anorexia or cachexia, comprises contacting cell expressing mammalian Ob

PT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test

PT compound

XX Claim 1; Fig 3; 109pp; English.

PS The patent discloses obese receptor (ObR) proteins and nucleic acids

XX encoding them. ObR protein participates in the regulation of mammalian

CC body weight. The invention also relates to a method of identifying

CC therapeutic compounds for the treatment of a body weight disorder.

CC The method involves contacting a cell that expresses a mammalian ObR

CC protein, a JAK2 protein and a mammalian SOCS-1 protein with a test

CC compound. The method is useful for identifying compounds which modulate

CC ObR gene expression and gene product activity, which can be used as

CC agents to control body weight particularly as therapeutic agents for

CC treating body weight disorders, including obesity, cachexia and anorexia.

CC The present sequence is ObR protein from human.

XX

SQ Sequence 1165 AA;

Query Match 100.0%; Score 6254; DB 22; Length 1165;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWFKLSKMPNSTYDYFLLPAGLSKNTSNS 60

Db 1 micqkfvcvllhwefiyvitafnlsypitpwrklskmpnstydyfllpaglskntsns 60

QY 61 NGHYETAPEKFNSSGTHFSNLSKTTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120

Db 61 nghyetavepkfnssgthfsnlskttfhccfrseqrncslcadniegkttfstvnslvf 120

QY 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFNRYNYKVHLLYVLPVEVLESPVPQKGS 180

Db 121 qqidanwniqcwlkglklficyveslfknlfrynnykvhllylvlevedsylvpqqgs 180

QY 181 FQMVHCNCSVHECECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINVMVKPDP 240

Db 181 fqmvhcnscvhecececlvpvptaklndtlmlclkitsggvifqspmsvqpinvmvkpdp 240

QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVYKSENSTTVIREADKIVSATSLLVDSILP 300

Db 241 lglhmeitddgnlkiswsspplvpfploqyqvysensttvireadkivsatsllvdsilp 300

QY 301 GSSYEVQVRGKRLDGPINSDWSTPRVFTTQDVIYFPFKILTSGSNVSHCIYKKENKI 360

Db 301 gssyevqvrgrldgpgiwsdwstprvfttqdvlyfppkiltsgsnvshfciykkenki 360

QY 361 VPSKEIVVMNLAEKIPQSYDVVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420

Db 361 vpskeivvmnlaekipqsydvvsdhvskvtfnlnetkprgkftydavycnehechh 420

QY 421 RYAEIYVIDVNIINISCECTDGYLTMTCTRWSSTIQLSLAESTLQLRYHRSLSYCSIDPSIH 480

Db 421 ryaelyvidvniiniscetdgyltkmtcrwststqlslaestlqlryhrsslycsidpsih 480

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540

Db 481 pisepkdcylqsdgfyecifqipflllsgytwirinhslgldspptcvlpdsvvkplpp 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLQFIQIRYGLSGKEVQWKMYEVDKSKSVSLPV 600

Db 541 ssvkaeitinigllkiswekpvfpennlqfiqirylsgkevqwkmyevdsksvslpv 600

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

Db 601 pdlcavyavqvrckrldggywsnwsnpaytvvmdikvpmrgpefwrilingdtmkkeknv 660

QY 661 TLLWKPLMKNDLSQVQRVYVNHHTSCNGTWSDEVDGNHTKFTFLWTEQAHTVTVLAINSI 720

Db 661 tllwkplmkndsicsvqrvynhhtscngtwsedvgnhtkftflwteqahtvtvlainsi 720

QY 721 GASVANFNLTFSPWMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780

Db 721 gasvanfntlfsmpmskvnivqslsayplnsscvivswilspdyklyfiiewknlne 780

QY 781 GEIKWLRISSSVKYYIHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840

Db 781 geikwlrisssvkkyyihdfiipiekqfslpiyfimegvgkpkkinsftqddiekhqgsda 840

QY 841 GLYVIVPVISSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQLNFQKPETFEHLFI 900
|||||
Db 841 glyvivpviissilllgtllishqrmkklfwedvpnpkncswaglnfqkpetfehlf 900
|||||
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPTTWVSLSTTDLEKGSVCISDQFN 960
|||||
Db 901 khtasvtcgp1llepetisedisvdtswknkdemmpttvvslsttdlekgsvcisdqfn 960
|||||
QY 961 SVNFSEAGTEVTEDESQRQPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSPL 1020
|||||
Db 961 svnfseagtevyedesqrqpfvkyaatlisnspsetgeeqlinssvtkcfssknspl 1020
|||||
QY 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
|||||
Db 1021 kdsfnssweieaqaffilisdqhpniisphltfseglde1llklegnfpeenndkksiiyl 1080
|||||
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFFAS 1140
|||||
Db 1081 gvtsikkresgvlltdksrvscppapclftdirvlqdschfvenninlgtsskktffas 1140
|||||
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
|||||
Db 1141 ympqfqtctstqthkimenkmcldtv 1165
|||||
RESULT 3
AAW34500
ID AAW34500 standard; protein; 1220 AA.
XX
AC AAW34500;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor D protein.
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..1165 /note= "encoded by AAT98531"
FT Misc-difference 1166 /label= unknown
FT Misc-difference 1169 /note= "encoded by stop codon"
FT Misc-difference 1187 /label= unknown
FT Misc-difference 1187 /note= "encoded by stop codon"
FT Misc-difference 1207 /label= unknown
FT Misc-difference 1207 /note= "encoded by stop codon"
FT Misc-difference 1..1165 /note= "encoded by AAT98531"
XX
PN WO9725424-A1.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US00128.
XX
PR 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX
PA (AMGE-) AMGEN INC.
XX Chang M, Fletcher FA, Welcher AA;
XX WPI; 1997-384981/35.
DR

DR N-PSDB; AAT98531.
XX
PT Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol or blood lipid levels
PT
XX
PS Claim 31; Page 76; 151pp; English.
XX
CC This sequence represents the obesity (OB) receptor D protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.
XX
SQ Sequence 1220 AA;

Query Match 100.0%; Score 6254; DB 18; Length 1220;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSOMPNNSTYDYFLLPAGLSKNTSNS 60
|||||
Db 1 micqkfcvllhwefiyvitafnlsypitpwrfklsompnnstydyfllpaglskntsns 60
|||||
QY 61 NGHJETAVEPKFNSSGTHFNSLSKTTFFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
|||||
Db 61 nghjetavepkfnssgthfnslskttfhccfrseqdrncslcadniegkftfstvnslvf 120
|||||
QY 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS 180
|||||
Db 121 qqidanwniqcwlkgdlkfcyveslfnlfrnrykvhllylvpvledsplyvpqkgs 180
|||||
QY 181 FQMVHCNCSVHECCVLPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDP 240
|||||
Db 181 fqmvhcnscvheccvlpvptaklndtllmclkitsggvifqsplmsvqpinmvpdp 240
|||||
QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
|||||
Db 241 lglhmeitddgnlkswsspplvpfploqyvkysensttvireadkivsatsllvdsilp 300
|||||
QY 301 GSSYEVQVRGKRLDGPGLIWSDMSTPRVFTTQDVIYFPFKILTSGVSNVSFHCIVKKNKI 360
|||||
Db 301 gssyevqvrgrldgpgiwsdwstprvfttqdvifppkiltsvgsnvsfhciykenki 360
|||||
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFNLTNETHKPRGKFTYDAVYCCNEHECHH 420
|||||
Db 361 vpskeivwmnlaekipqsgydvvsdhvskvtfnnltnethkprgkftydavycnehechh 420
|||||
QY 421 RYAEELYVIDVNIINISCEYDGYLTMTCRWSTSTTQSLAESTLQLRYHRSLSLYCSDIPSIIH 480
|||||
Db 421 ryaelyvldvnniniscetdgyltkmtcrwststtqslaestqlryhrsslycsdipsih 480
|||||
QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
|||||
Db 481 ptsepkdcylqsdgfyecifqipifllsgytmwirinhslgsldspptcylpdsvvkplpp 540
|||||
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEVDKSKSVSLPV 600
|||||
Db 541 ssvkaeitinigllkiswekpvfpennlqfiryglsgkevqwkmyevdaksksvslpv 600
|||||
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
|||||
Db 601 pdlcavavqvrckrldglgywsnwnsnpaytvvmdikvpmrgpefwrilingdtmkkeknv 660
|||||
QY 661 TLLWKPLMKNDLSQVQRYVINHHTSCNGTWSVEDYGNHTKFTFLWTEQAHTVTVLAINSI 720
|||||
Db 661 tllwkplmkndslsqvqryvinhhtscngtwsedvgnhtkftflwteqahtvtvlainsi 720
|||||
QY 721 GASVANFNLTFSWPMKYNIVQSLSAYPLNSSCVIYSWILSPSDYKLMYFIIEWKNLNED 780
|||||

Db 721 gasvanfntfswpmksknivqslsayplnsscvivswilspdyklmyfiiewknlnd 780

QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIEMGVGPKKIINSFTQDDIEKHQSDA 840

Db 781 geikwlriSSSVKKYYIHDHFIPIEKYQFSLYPIEMGVGPKKIINSFTQDDIEKHQSDA 840

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPEFHLFI 900

Db 841 glyvivpviSSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPEFHLFI 900

QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDMMPTTVVSLSTTDLEKGSVCISDQFN 960

Db 901 khtasvTCGPLLEPETISEDISVDTSWKNKDMMPTTVVSLSTTDLEKGSVCISDQFN 960

QY 961 SVNFSEAEGETVYEDESQRPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020

Db 961 svnfseaeGETVYEDESQRPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020

QY 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENDRKSIYYL 1080

Db 1021 kdsfnsSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENDRKSIYYL 1080

QY 1081 GVTSIKKRESGVLLTDKSRVSCFPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140

Db 1081 gvtsikkRESGVLLTDKSRVSCFPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140

QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

Db 1141 ympqfQTCSTQTHKIMENKMCDLTV 1165

RESULT 4

AAE12551

ID AAE12551 standard; Protein; 1165 AA.

XX

AC AAE12551;

XX 03-JAN-2002 (first entry)

XX Human Ob receptor (ObR) protein mutant (Y1141F).

DE Human; obese receptor; ObR; anorectic; anabolic; body weight disorder;

XX therapy; obesity; cachexia; anorexia; mutant; mutein.

KW Homo sapiens.

XX Synthetic.

OS Key

OS Peptide

FT Location/Qualifiers

FT 1..20

FT /label= Signal_peptide

FT 21..1165

FT /label= Human_mature_ObR_protein

FT 21..839

FT /label= Extracellular_domain

FT 23..25

FT /note= "Asn is N-glycosylated"

FT 41..43

FT /note= "Asn is N-glycosylated"

FT 56..58

FT /note= "Asn is N-glycosylated"

FT 59..61

FT /note= "Asn is N-glycosylated"

FT 73..75

FT /note= "Asn is N-glycosylated"

FT 98..100

FT /note= "Asn is N-glycosylated"

FT 187..189

FT /note= "Asn is N-glycosylated"

FT 206..208

FT /note= "Asn is N-glycosylated"

FT 276..278

FT /note= "Asn is N-glycosylated"

FT 347..349

FT Region /note= "Asn is N-glycosylated"

FT 319..323

FT /note= "Conserved motif of cytokine I receptor family"

FT 397..399

FT /note= "Asn is N-glycosylated"

FT 433..435

FT /note= "Asn is N-glycosylated"

FT 516..518

FT /note= "Asn is N-glycosylated"

FT 622..626

FT /note= "Conserved motif of cytokine I receptor family"

FT 624..626

FT /note= "Asn is N-glycosylated"

FT 659..661

FT /note= "Asn is N-glycosylated"

FT 670..672

FT /note= "Asn is N-glycosylated"

FT 688..690

FT /note= "Asn is N-glycosylated"

FT 697..699

FT /note= "Asn is N-glycosylated"

FT 728..730

FT /note= "Asn is N-glycosylated"

FT 750..752

FT /note= "Asn is N-glycosylated"

FT 840..862

FT /label= Transmembrane_domain

FT 863..1165

FT /label= Cytoplasmic_domain

FT Misc-difference 1141

FT /note= "Wild type Tyr substituted with Phe"

XX

XX US6287782-B1.

XX 11-SEP-2001.

XX 29-APR-1998; 98US-0069781.

XX 27-NOV-1995; 95US-0562663.

XX 04-DEC-1995; 95US-0566622.

XX 08-DEC-1995; 95US-0569485.

XX 11-DEC-1995; 95US-0570142.

XX 28-DEC-1995; 95US-0583153.

XX 22-JAN-1996; 96US-0599455.

XX 26-APR-1996; 96US-0638524.

XX 03-SEP-1996; 96US-0708123.

XX 28-MAY-1997; 97US-0864564.

XX (MILL-) MILLENNIUM PHARM INC.

PA Tartaglia LA, Tepper RI, Culpepper JA, White DW;

PI WPI; 2001-624489/72.

XX Identifying compounds for treating body weight disorder, e.g. obesity, anorexia or cachexia, comprises contacting cell expressing mammalian Ob receptor protein, JAK2 protein and mammalian SOCS-1 protein with test compound -

XX Disclosure; Page -: 109pp; English.

XX The patent discloses obese receptor (ObR) proteins and nucleic acids encoding them. ObR protein participates in the regulation of mammalian body weight. The invention also relates to a method of identifying therapeutic compounds for the treatment of a body weight disorder. The method involves contacting a cell that expresses a mammalian ObR protein, a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The method is useful for identifying compounds which modulate ObR gene expression and gene product activity, which can be used as agents to control body weight particularly as therapeutic agents for treating body weight disorders, including obesity, cachexia and anorexia. The present sequence is human ObR protein mutant (Y1141F).

CC Note: This sequence is not shown in the specification but is derived

CC from the wild-type human Obr protein shown in figure 3 of the
CC specification (AAE12609).

XX Sequence 1165 AA;

Query Match 99.9%; Score 6250; DB 22; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MICQKFCVLLHWEFIYVITAFNLSPYITPWRFKLSMPNPNSTYDYFLLPAGLSKNTSNS	60
Db	1	micqkfcvllhwefiyvitafnlspypitpwrflksmpnpnstydyfllpaglskntsns	60
QY	61	NGHYETAPEPKFNSSGTHFNSLSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	nghyetavepkfnssgthfnslsttfhccfrseqdrncslcadniegktfvstvnslvf	120
QY	121	QQIDANWNIQCWLKGDLLKFLFICVYESLFKNLFRNRYNYKVHLLYVLPFVLEDSPVPQKS	180
Db	121	qqidanwniqcwlkgdllkflficyveslfknlfrnynykvhllylvlpevledsplvpqks	180
QY	181	FQMVHCNCSVHECECLVPVPTAKLNDTLMLCLKITSGGVTFOSPLMSVQPINMVKPDPP	240
Db	181	fqmvhcncsvhecceclvpvptaklndtlmlclkitsggvtfosplmsvqpinmvkpdpp	240
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVYKYSNSTTIREADKIVSATSLLVDSILP	300
Db	241	lglhmeitddgnlkiwsspplpvpfpplqyqvkysesttireaakivsatsllvdsilp	300
QY	301	GSSYEQVGRKRLDGPGLWDSWSPRVFTQDVYFPPKILTSVGSNVSEHCYKKNKI	360
Db	301	gssyeqvgvrgkrlldgpglwsdswsprvftqdvlyfppkiltsvgsnvsefciykkenki	360
QY	361	VPSKEIYVWMMNLAEKIPQSQDYVDVSDHVSQVTFNLTNETPKCKFTYDAVYCCNEHECH	420
Db	361	vpskeiyvwmnlaekipqsqdyvdsdhvskvtfnltnetpkckfthydavyccnehechh	420
QY	421	RYAELYVIDVNNINISCETDGYLTMTCTRWSTSTIQSLAESTLQLRYHRSSLYCSDIPS	480
Db	421	ryaelyvidvnniniscetdgyltkmtcrwststiqslaestlqlryhrsslycsdipsih	480
QY	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP	540
Db	481	pisepkdcylqsdgfyecifqipifllsgytmwirinhsllgsldspptcvlpdsvvkplpp	540
QY	541	SSVKAETITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMVEYDAKSWSLVP	600
Db	541	ssvkaeitinigllkiswekvpfpennlfqiryglsgkevqwkmyevydaaksksvslpv	600
QY	601	PDLCAVAVQVRCKRLDGLGYWNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKERNV	660
Db	601	pdlcavavqvrckrldglgywnsnpnpaytvvmdikvpmrgpefwriingdtmkkernv	660
QY	661	TLWKPLMKNDLSCSVQVRVYVNHHTSCNGTWSQVSDVGNHTKFTFLWTEQAHTVTVLAIN	720
Db	661	tllwkplmkndslcsvgvryvnhhtscngtwsedvgnhtkftflwteqahtvtvlainsi	720
QY	721	GASVANFNLTFSWPMSKVNIQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEWKLNED	780
Db	721	gasvanfnltfswpmskvniqslasayplnsscvivswilspdsydklmyfielwknined	780
QY	781	GEIKWLRISSSVKKYYIHDHPIPIEKYQFSLYPIFMEGVGPKKIINSFTQDDIEKHQSDA	840
Db	781	geikwlri:sssvkkyihdhpiipiekqfslypifmegvgpkkiinsftqddiekhsda	840
QY	841	GLYIVPVVPISSSILLGLTLLISHQRMKKLFWEVDPNPKNCSSWAQGLNFQKPEFHLFI	900
Db	841	glyivpvvi:sssillgltllishqrmkklfwevdpnpknscswaaglnfqkpetfehlf	900
QY	901	KHTASVTCGPLLLEPETISEDITSVDTSWKNKDEMPTTVVSLSTTDLEKSGSVCISDQFN	960
Db	901	khtasvtcgpplllepmetisedsivdtswnkdempttvvslsttdleksgsvcisdqfn	960

QY	961	SVNFSEABGTEVTEYDESRQPFVKYATLISNSKPSKSETGEEGLINSSVTKCFSSKNSPL	1020
Db	961	svnfseagtevtetyedesqrqpfvkyatlisnkskpsksetgeeglinssvtkcfssknspl	1020
QY	1021	KDSFSNSSWEIEAQAFILSDQHNPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL	1080
Db	1021	kdsfnsnwieieaqafilsdqhnpniisphltfsegldeallklegnfpeenndkksiiyl	1080
QY	1081	GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS	1140
Db	1081	gvtsikkresgvlltdksrvscppfapclftdirvlqdschfvenninlgtsskktfas	1140
QY	1141	YMPQFQTCSTQTHKIMENKMCDLTV	1165
Db	1141	ympqfqtctstqthkimenkmcldtv	1165

RESULT 5
AAY13474

ID AAY13474 standard; Protein; 1165 AA.

XX AC AAY13474;

XX DT 26-JUL-1999 (first entry)

XX DE Peptide Seq ID No: 4-of-WO9923493..

XX KW Leptin; phosphorylated leptin receptor; tyrosine phosphatase 1D; PTP-1D;
XX KW modulator; drug; weight loss; adiposity; hypertension; heart disease;
XX KW type II diabetes; cancer; AIDS; agriculture.

XX OS Homo sapiens.

XX PN WO9923493-A1.

XX PQ 14-MAY-1999.

XX PF 27-OCT-1998; 98WO-US22797.

XX PR 26-OCT-1998; 98US-0178691.

XX PR 31-OCT-1997; 97US-0961809.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PI Friedman JM, Li C;

XX WPI; 1999-327025/27.

XX DR N-PSDB; AAX55588.

XX PT Identifying modulators agents that modulate leptin activity

XX PS Disclosure; Page 77-84; 95pp; English.

XX CC The invention provides a method for identifying modulators of binding of
CC a phosphorylated leptin receptor with tyrosine phosphatase 1D (PTP-1D).
CC The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin
CC receptor or its phosphorylated fragment with protein PTP-1D or its
CC fragment in the presence and absence of a candidate agent under
CC conditions in which the absence of the agent the binding of the
CC phosphorylated leptin receptor or fragment with PTP-1D or its fragment
CC can be detected; and (b) detecting the binding of the phosphorylated
CC leptin receptor and PTP 1D; where an increase in binding detected in the
CC presence of the agent, indicates that the agent enhances binding, and a
CC decrease in binding in the presence of the agent indicates that the agent
CC is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin
CC receptor-dependent PTP-1D phosphorylation are useful as drugs in weight
CC loss diet regimens. The drugs identified can regulate adiposity and fat
CC content of animals, particularly in mammals. Disorders that can be
CC treated by PTP-1D modulators include obesity and its associated diseases,
CC e.g. hypertension, heart disease and type II diabetes, and weight loss
CC associated with cancer and AIDS. Additionally the agents identified may
CC be useful in agriculture where body weight of domestic animals can be

QY	961	SVNFSEAGTEVTYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL	1020
Db	961	svnfseagtevtYeasqrpfvkyatlisnkskpsetgeeglinssvckcfssknspl	1020
QY	1021	KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYYL	1080
Db	1021	kdsfsnssweieaqafilsdqhpniiisphltfsegldeallklegnfpeennndkksiiyy1	1080
QY	1081	GVTSIKKRESGVLITDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS	1140
Db	1081	gvtsikkresgvlitdksrvcfpapclftdirvlqdcshfvenninltsskkktfas	1140
QY	1141	YMPQFQTCSTQTHKIMENKMCDLTV	1165
Db	1141	ympqfqtctstqthkimenkmcldtv	1165
RESULT 6			
AAW19116			
ID	AAW19116	standard; Protein; 1165 AA.	
XX	XX	AAW19116;	
DT	26-AUG-1997	(first entry)	
XX	XX	Human Ob receptor.	
DE	DE		
XX	XX		
KW	KW	Ob receptor; Obr; cytokine receptor; signal transduction;	
KW	KW	eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;	
KW	KW	therapy.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
FH	FH	Key	Location/Qualifiers
Peptide	Peptide	1..20	/label= Sig_peptide
FT	FT	21..839	/label= ECD
Domain	Domain	/note= "extracellular domain"	
FT	FT	840..862	/label= TMD
FT	FT	/note= "transmembrane domain"	
Domain	Domain	863..1165	/label= CD
FT	FT	/note= "cytoplasmic domain"	
Peptide	Peptide	319..323	/note= "motif conserved in class I cytokine receptors"
FT	FT	622..626	/note= "motif conserved in class I cytokine receptors"
Modified-site	Modified-site	23	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	
Modified-site	Modified-site	41	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	
Modified-site	Modified-site	59	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	
Modified-site	Modified-site	98	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	
Modified-site	Modified-site	187	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	
Modified-site	Modified-site	206	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	
Modified-site	Modified-site	276	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	
Modified-site	Modified-site	347	/label= Glycosylation
FT	FT	/note= "potential N-linked glycosylation site"	

FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 433 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 516 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 624 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 658 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 670 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 688 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 697 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 728 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
FT 750 Modified-site
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"

WO9719952-A1.
05-JUN-1997.
27-NOV-1996; 96WO-US19128.
03-SEP-1996; 96US-0708123.
27-NOV-1995; 95US-0562663.
04-DEC-1995; 95US-0566622.
08-DEC-1995; 95US-0569485.
11-DEC-1995; 95US-0570142.
28-DEC-1995; 95US-0583153.
22-JAN-1996; 96US-0599455.
26-APR-1996; 96US-0638524.
(MILL-) MILLENNIUM PHARM INC.
Culpepper JA, Tartaglia LA, Tepper RI, White DW;
WPI; 1997-310525/28.
N-PSDB; AAT69592.

Isolated Ob receptor genes and polypeptide(s) - useful to develop products for diagnosis or treatment of body weight disorders, e.g. obesity, cachexia, anorexia and bulimia
Example; Fig 3; 265pp; English.

Human Ob receptor (OBR) (AAW19116) is a novel polypeptide that participates in the control of body weight and which is involved in signal transduction triggered by the binding of its natural ligand, Ob (leptin). It is a member of the class I cytokine receptor family. Its amino acid sequence was deduced from a foetal brain cDNA clone (AAT69592). The receptor corresponds to the long form mouse OBR (AAW19115). OBR proteins, peptides, antibodies, agonists and antagonists can be used in the diagnosis and treatment of body weight disorders such as obesity, cachexia and anorexia.

Sequence 1165 AA;

Query Match 99.8%; Score 6240; DB 18; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	1	MICQKFCVWLLHWEFIYVITAFNLSPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNTSNS	60	
Db	1	micqkfcvllhwefiyvitafnlspitpwrklsclmpnnydyfllpaglskntsns	60	
QY	61	NGHYETAPEPKFNSSGTHFSNLSTKTHCCFRSEQDRNCSICADNIEGKTFVSTVNSLVE	120	
Db	61	nghyetavepkfnssgthfslskttfhccfrseqdrncalcadniegktfstvtnslvf	120	
QY	121	QQIDANWNIQCWLKGDCLKFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS	180	
Db	121	qqidanwniqcwlkgdclkficyveslfknlfrnrynykvhllyvlpvleedsplvpqkgs	180	
QY	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP	240	
Db	181	fqmvhcnscsvhecceclvpvptaklndtllmclkitsggvifqspmlmsvqipnmvkdpp	240	
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPLOYQYQVYSENSTTVIREADKIVSATSLLVDSILP	300	
Db	241	lgihmeitddgnlkiwsspplpvpfploiyqvysensttvireadkivsatsllvdsilp	300	
QY	301	GSSYEVQVRGKRLDGPISWSDWSTPRVFTTQDVIYFPKILTSGVSNVSFHCYKKNKI	360	
Db	301	gsseyevqvrgrldgpgiwsdwstprvfttqdvifypkiltsgvsnvsfhclykknki	360	
QY	361	VPSKEIVWMNLAEKIPQSOYDVVDVSHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH	420	
Db	361	vpskeivwmnlaeikpgsydvvdvshvskvtffnlnetkprgkftydavycnehechh	420	
QY	421	RYAELVVIDVNNINISCETDGYLTMTKTCRSTSTIQSLAPSTLQRLYHRSSLYCSDIPSIH	480	
Db	421	ryaelvvidvnniniscetdgyltkmtcrststiqslaestlqlryhrsslycsdipsih	480	
QY	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVVKPLPP	540	
Db	481	pisepkdcylqsdgfyecifqipifllsgytmwirinhslgslldpctcvlpdsvvkplsp	540	
QY	541	SSVKAEBITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV	600	
Db	541	ssvkaeitinigllkislekpvfpennlqfiryglsgkevqwkmyevydaksksvslpv	600	
QY	601	PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660	
Db	601	pdlcavayavqvrckrldglgywsnwsnpaytvvmdikvpmrgpefwrilingdtmkkeknv	660	
QY	661	TLLWKPLMKNDSLCSVORYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTVLAINSI	720	
Db	661	tlwkplmkndslcsvqrvyinhhtscngtwsdevgnhtkftflwteqahtvtvlainsi	720	
QY	721	GASVANFNLTFSWPMKVNIVQSLAYSAPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED	780	
Db	721	gasvanfnltfswpmkvnivqslaysaplnsscvivswilspdyklymfiiwknlned	780	
QY	781	GEIKWLRISSSVKKYVIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA	840	
Db	781	geikwlrisssvkkyyihdhfipiekyyqfslypifmegvgkpkinsftqddiekhqsd	840	
QY	841	GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPFTEHLFI	900	
Db	841	glyvivpviisslllgtllishqrmkklfwedvpnpknscswaqglnfqkpetfehlf	900	
QY	901	KHTASVTCGPLLLEPETISEDIVSDTSWKNKDEMMPTTVVSLSTTDLEKGSVCISDQFN	960	
Db	901	khtasvtcgplllepetisedivsdtswnkndemmttvvslsttdlekgsvcisdqfn	960	
QY	961	SVNFSEAEGETVYEDESQRPVVKYATLISNSKPSSETGEEQGLINSVTKCFSSKNSPL	1020	
Db	961	svnfseaegetvtyedesqrpfvkyaatlisnspsetgeegqlinsvtkcfssknspl	1020	
QY	1021	KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNKKSIYYL	1080	
Db	1021	kdsfsnssweieaqaffilsdqhpniisphltfsegldeillklegnfpeenndkksiyyl	1080	

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Db 179 TFSWKY-----KNSDISSTRGFPSPVLRGGKYATSQVLLPSKDVMOQTDEH 225
QY 228 --CNSRDSNGN 236
Db 226 VVCKVQHNGN 236

RESULT 11
Q9BRV0
ID Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 54.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 33.9%; Score 450.5; DB 4; Length 500;
Best Local Similarity 69.0%; Pred. No. 7.2e-29;
Matches 89; Conservative 9; Mismatches 28; Indels 3; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVHLVQSGAEVMSPGASVRVCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSDNTRF 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AQKFQGRVTMTSDTSGTAYMELSLRSSDDTAVYYCARDRY--YGSAYHRGSYYMDVWG 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 AKKFQGRVTLTDTSTSTVMELSLRLSDDTAVYYCAR-RYCSYSSQNDYYYYMDVWG 138
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 119 RGTLTIVSS 127
Db 139 KGTTIVSS 147

RESULT 12
Q9GYZ2
ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 33.9%; Score 450; DB 5; Length 119;
Best Local Similarity 67.7%; Pred. No. 1.4e-29;
Matches 86; Conservative 13; Mismatches 20; Indels 8; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGAEVKKPGASVRVCKASGYTFGTGYMYWVRQAPGCHGLEWIGYINPSRGYTN 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AQKFQGRVTMTSDTSGTAYMELSLRSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFQGRVTMTDTKSFSTAYMDLRLSLRSADSAVYYCAR-----YDDHYCLDYWGQG 112
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TLVTVSS 127
Db 113 TTVTVSS 119

RESULT 13
Q9QXE9
ID Q9QXE9 PRELIMINARY; PRT; 117 AA.
AC Q9QXE9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 32.6%; Score 433; DB 11; Length 117;
Best Local Similarity 64.6%; Pred. No. 3.4e-28;
Matches 82; Conservative 17; Mismatches 18; Indels 10; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFDTYMKWVKQSHGKSLEWIGDINPNNGGT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 16:36:09 ; Search time 28.14 Seconds
(without alignments)
342.614 Million cell updates/sec

Title: US-08-779-457-48

Perfect score: 1329

Sequence: 1 EVQLVQSGAEVKKPGASVKV.....SRDSSGNHVVFGGFKLTVL 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	521	39.2	108	1	LV3A_HUMAN	P01714 homo sapien
2	483	36.3	117	1	HV1G_MOUSE	P23083 homo sapien
3	479.5	36.1	147	1	HV1C_HUMAN	P01744 homo sapien
4	443	33.3	117	1	HV1B_HUMAN	P01743 homo sapien
5	434	32.7	117	1	HV13_MOUSE	P01757 mus musculus
6	429.5	32.3	139	1	HV07_MOUSE	P01751 mus musculus
7	420	31.6	117	1	HV12_MOUSE	P01756 mus musculus
8	415	31.2	120	1	HV03_MOUSE	P01747 mus musculus
9	411	30.9	140	1	HV02_MOUSE	P01746 mus musculus
10	410.5	30.9	120	1	HV50_MOUSE	P06329 mus musculus
11	403.5	30.4	118	1	HV51_MOUSE	P06330 mus musculus
12	395.5	29.8	137	1	HV11_MOUSE	P01755 mus musculus
13	385	29.0	121	1	HV01_MOUSE	P01745 mus musculus
14	381	28.7	138	1	HV48_MOUSE	P03980 mus musculus
15	380.5	28.6	114	1	HV00_MOUSE	P01741 mus musculus
16	377	28.4	111	1	LV3B_HUMAN	P80748 homo sapien
17	376	28.3	117	1	HV1A_HUMAN	P01742 homo sapien
18	368	27.7	117	1	HV09_MOUSE	P01753 mus musculus
19	366	27.5	107	1	LV4C_HUMAN	P01717 homo sapien
20	366	27.5	117	1	HV04_MOUSE	P01748 mus musculus
21	364	27.4	108	1	LV5A_HUMAN	P01719 homo sapien
22	363	27.3	106	1	LV4A_HUMAN	P01715 homo sapien
23	361.5	27.2	120	1	HV1H_HUMAN	P80421 homo sapien
24	361	27.2	136	1	HV15_MOUSE	P01759 mus musculus
25	360	27.1	117	1	HV06_MOUSE	P01750 mus musculus
26	358	26.9	106	1	LV4B_HUMAN	P01716 homo sapien
27	356	26.8	106	1	LV4E_HUMAN	P06889 homo sapien
28	355	26.7	117	1	HV49_MOUSE	P06328 mus musculus
29	353	26.6	125	1	HV1F_HUMAN	P06326 homo sapien
30	352	26.5	117	1	HV10_MOUSE	P01754 mus musculus
31	352	26.5	117	1	HV14_MOUSE	P01758 mus musculus
32	349.5	26.3	119	1	HV38_MOUSE	P01808 mus musculus
33	348.5	26.2	119	1	HV37_MOUSE	P01807 mus musculus

ALIGNMENTS

RESULT 1

LV3A_HUMAN
ID LV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01714;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-III region SH.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 245:2171-2176(1970).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01980; L3HUSH.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 21 86
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 39.2%; Score 521; DB 1; Length 108;

Best Local Similarity 92.5%; Pred. No. 2e-32;

Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 143 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQQKPGQAPVLYIGKNNRPSGIPDRF 202
|||||
Db 1 SELTQDPAVSVALGQTVRITCGDSLRSYDAAWYQQKPGQAPVLYIGRNNRPSGIPDRF 60

QY 203 SGSSSGNTASLTITGAQAEDEADYVNSRDSSGNHVVFGGFKLTVL 249
|||||
Db 61 SGSSSGHTASLTITGAQAEDEADYVNSRDSSGKHVLFGGGFKLTVL 107

RESULT 2

HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;

DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RL heavy-chain locus";
RL EMBO J. 7:1047-1051(1988).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 36.3%; Score 483; DB 1; Length 117;
Best Local Similarity 92.9%; Pred. No. 1.4e-29;
Matches 91; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGYYMWVVRQAPGQGLEWMGWINPNSGGTNY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFGYYMWVVRQAPGQGLEWMGRINPNSGGTNY 79
QY 61 AQKFGQRTVTMTDTSIGTAYMELSLRLSSDDTAVYYCAR 98
Db 80 AQKFGQRTVTMTDTSISTAYMELSLRLSSDDTAVYYCAR 117

RESULT 3
HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.

DR PIR; A02026; EIHUND.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 36.1%; Score 479.5; DB 1; Length 147;
Best Local Similarity 69.5%; Pred. No. 3.3e-29;
Matches 89; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGYYMWVVRQAPGQGLEWMGWINPNSGGTNY 60
Db 20 QTQLVQSGAEVKKPGASVKVSCKASGYTFDYSIHQIRQAPGHGLEWMGWINPNSGGTNY 79
QY 61 AQKFGQRTVTMTDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRG-SYYMDVWGR 119
Db 80 APRFGQRTVTMTDTSFSTAYMDLRLSRSDSDSAVFYCAKSDPFWSYDYNFDYSYTLDVWGO 139

QY 120 GTLVTVSS 127
Db 140 GTTVTVSS 147

RESULT 4
HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
RN [2]
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CC -----
CC EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVH0HG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.


```
Db 20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY 79
QY 61 AQKFQGRVTMTSDTSIGTAYMELSLSSDDTAVYYCARDRIYGGSSAYHRGSIYMDVWGSG 120
Db 80 NEKFKGKTTLTVDKSSSTAYMQLSLTSEDSAVYFCARSHYYG-----GSYDFDYWGQG 133
QY 121 TLVTVSS 127
Db 134 TPLTVSS 140

RESULT 10
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 30.9%; Score 410.5; DB 1; Length 120;
Best Local Similarity 59.8%; Pred. No. 3.5e-24;
Matches 76; Conservative 18; Mismatches 26; Indels 7; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYVWRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 QVQLLPQGTTELKPGASVNLSCASGYTFTSYWMHWIRQRPQGQLEWIGGINPSNGGTNY 60

QY 61 AQKFQGRVTMTSDTSIGTAYMELSLSSDDTAVYYCARDRIYGGSSAYHRGSIYMDVWGSG 120
Db 61 NEKFKSKATLTVDKSSSTAYMQLSTPTSEDSAVYYCARWDY-----EGDRYFDVWGSG 113

QY 121 TLVTVSS 127
Db 114 TTVTVSS 120

RESULT 11
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 30.4%; Score 403.5; DB 1; Length 118;
Best Local Similarity 62.2%; Pred. No. 1.1e-23;
Matches 79; Conservative 15; Mismatches 24; Indels 9; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYVWRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYMYMVVKQSHGKSLEWIGDINPNNGGTSY 60

QY 61 AQKFQGRVTMTSDTSIGTAYMELSLSSDDTAVYYCARDRIYGGSSAYHRGSIYMDVWGSG 120
Db 61 NQKFKGKATLTVDKSSSATYMELSLTSEDSAVYYCARG--YGYDPF-----DVMGTG 111

QY 121 TLVTVSS 127
Db 112 TTVTVSS 118

RESULT 12
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC
CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
CC InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5681BF44B8EC9 CRC64;

Query Match 29.8%; Score 395.5; DB 1; Length 137;
Best Local Similarity 59.8%; Pred. No. 5.2e-23;
Matches 76; Conservative 17; Mismatches 25; Indels 9; Gaps 2;

Qy 1 EVQLVQSGAEVKKPGASVKVSCKASGYFTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 20 QVQLQQPGAEFVKPGASVKLSCKASGYFTSYLMHWYNQRPGRGLEWIGRIDPNSSGGTTY 79

Qy 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120
Db 80 NEHFRSKATLTIDKPSSTAYMQLSLSLTSSEDSAVYYCAR-----YRLGRYF-DYWGGQ 130

Qy 121 TLVTVSS 127
Db 131 TTLTVSS 137

RESULT 13
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 29.0%; Score 385; DB 1; Length 121;
Best Local Similarity 55.9%; Pred. No. 2.7e-22;
Matches 71; Conservative 21; Mismatches 29; Indels 6; Gaps 1;
```

```
Qy 1 EVQLVQSGAEVKKPGASVKVSCKASGYFTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 EAQLQQSGAELVRPGTSVKISCKAAGYFTTNYWIGWKERPGHGLEWIGDIYPGGGFTNY 60

Qy 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120
Db 61 NDNLKGKATLTADTSSSTAYIQLSLSLTSSEDSAIYHCARGIYNNSSP-----YFDSWGQG 114

Qy 121 TLVTVSS 127
Db 115 TTLTVSS 121

RESULT 14
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 28.7%; Score 381; DB 1; Length 138;
Best Local Similarity 57.0%; Pred. No. 6.2e-22;
Matches 73; Conservative 21; Mismatches 24; Indels 10; Gaps 2;

Qy 1 EVQLVQSGAEVKKPGASVKVSCKASGYFTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 20 QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWKQRPQGQGLEWIGEINPDGRSNY 79

Qy 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCAR-DRIYGGSSAYHRGSYYMDVWGR 119
Db 80 NEKFKNKATLTVDKSSSTAYMQLSLSLTPPEFAVYYCARSDGYDNFVY-----WGQ 130

Qy 120 GTLVTVSS 127
Db 131 GTLVTESA 138

RESULT 15
HV00_MOUSE
```

ID	HV00_MOUSE	STANDARD;	PRT; 114 AA.
AC	P01741;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	21-JUL-1986 (Rel. 01, Last annotation update)		
DE	Ig heavy chain V region (Anti-arsonate antibody).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE.		
RC	STRAIN=A/J;		
RX	MEDLINE=79195438; PubMed=109536;		
RA	Capra J.D., Nisonoff A.;		
RT	"Structural studies on induced antibodies with defined idiotypic		
RT	specificities. VII. The complete amino acid sequence of the heavy		
RT	chain variable region of anti-p-azophenylarsenate antibodies from A/J		
RT	mice bearing a cross-reactive idiotype.";		
RL	J. Immunol. 123:279-284(1979).		
CC	-1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF		
CC	THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V		
CC	REGION SEQUENCE.		
DR	PIR; A02022; GMSAA.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IGV; 1.		
KW	Immunoglobulin V region; Antiarsonate antibody.		
FT	NON_TER 114 114		
SQ	SEQUENCE 114 AA; 12555 MW; 99D8F0B6A69F4BE CRC64;		

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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:25:01 ; Search time 54.95 Seconds
(without alignments)
435.418 Million cell updates/sec

Title: US-08-779-457-48
Perfect score: 1329
Sequence: 1 EVQLVQSGAEVKKPGASVKV.....SRDSSGNHVVFGGKLTVL 249
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	635	47.8	268	A56446	Ig heavy chain V r
2	619.5	46.6	249	S41374	single chain Fv an
3	602	45.3	129	S46393	Ig heavy chain V r
4	569.5	42.9	233	JC5322	p53 specific singl
5	562	42.3	108	S47184	Ig lambda chain -
6	562	42.3	109	S19663	Ig lambda chain V
7	561	42.2	123	D33548	Ig heavy chain V-1
8	547.5	41.2	118	S36265	Ig heavy chain V r
9	546.5	41.1	135	S49530	anti-Sm antibody V
10	546	41.1	127	S70444	Ig lambda chain pr
11	545.5	41.0	110	S36272	Ig lambda chain V
12	535	40.3	108	S38498	Ig lambda chain -
13	533	40.1	109	S38496	Ig lambda chain -
14	531	40.0	171	S23623	Ig heavy chain V r
15	524	39.4	233	S25748	Ig lambda chain -
16	521	39.2	108	L3HUSH	Ig lambda chain V-
17	517.5	38.9	146	S02083	Ig lambda chain V-
18	512.5	38.6	110	S19672	Ig lambda chain V
19	507	38.1	98	S26938	Ig heavy chain V r
20	507	38.1	109	PH1668	Ig heavy chain V r
21	507	38.1	117	S18551	Ig heavy chain V r
22	503	37.8	96	S36060	Ig lambda chain -
23	503	37.8	115	S13726	Ig lambda chain V
24	502	37.8	233	S25741	Ig lambda chain -
25	499	37.5	98	S26912	Ig heavy chain V r
26	497	37.4	117	S31680	Ig heavy chain V r
27	495	37.2	142	A32483	Ig heavy chain V r
28	493.5	37.1	110	PH1669	Ig heavy chain V r
29	493	37.1	129	S36260	Ig heavy chain V r

30 491.5 37.0 136 2 S31600 Ig heavy chain V r
31 489 36.8 104 2 S69899 Ig heavy chain V r
32 488 36.7 126 2 I44151 Ig heavy chain V r
33 486 36.6 127 2 S34014 Ig heavy chain V r
34 483 36.3 117 1 HVHU35 Ig heavy chain pre
35 479.5 36.1 124 2 S19665 Ig heavy chain V r
36 479.5 36.1 143 1 E1HUND Ig heavy chain pre
37 468.5 35.3 120 2 S31999 Ig heavy chain V r
38 466.5 35.1 132 2 S31596 Ig heavy chain V r
39 465 35.0 131 2 S26792 Ig heavy chain V r
40 464 34.9 160 2 PL0105 anti-PR2 erythrocy
41 461 34.7 121 2 S20783 Ig heavy chain V r
42 461 34.7 127 2 PH0955 Ig heavy chain V r
43 459 34.5 122 2 S36271 Ig heavy chain V r
44 458.5 34.5 136 2 PH0960 Ig heavy chain V r
45 457.5 34.4 118 2 PH1666 Ig heavy chain V r

ALIGNMENTS

RESULT 1
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide
A:Reference number: A56446; MUID:95229583
A:Accession: A56446
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 635; DB 2; Length 268;
Best Local Similarity 51.6%; Pred. No. 4.7e-38;
Matches 131; Conservative 37; Mismatches 64; Indels 22; Gaps 6;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYFTFTGYIMVWVRQAPGQGLEWMGNPNSSGGTNY 60
Db 3 QVKLQESGAELVKPGASVKLSCTTSSTGTFNFKDTHHWVKRPEQGLEWIGRIAPANGITKY 62
QY 61 AQKFQGRVTMTSDTSIGTAYMELSLSSDDTAIVYVCARDRYYGSSAYHRGSYIM---DV 116
Db 63 DPKFQGKATIAADTSSNTAYLQLSSLTSEDVAVYCA-----SYLTRYENY 109
QY 117 WGRGTLTVSSGGGTGGGGGGSS-ELTQDPAY-SVALGQTVRITCGDLSRYSYAS 174
Db 110 WGQGTTVTVSSGGGGGGGGSDIETQSPAIMSASLGKVTMSCRASSSVN-FIY 168
QY 175 WYQOKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSRDSS 234
Db 169 WYQOKSDASPKLWVYVYTSHLPPGVPARFSGSGSGNSYSLTSSMEGEDAATYICQQTSS 228
QY 235 GNHVVFSGGKLTIV 248
Db 229 --PFTFGSGTKLEI 240

RESULT 2
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti

S19663
Ig lambda chain V region (clone alpha-BSA3) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19663
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A:Reference number: S19663; MUID:92085276
A:Accession: S19663
A:Molecule type: mRNA
A:Residues: 1-109 <MAR>
A:Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 562; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 SSELTDPAVSVALGQTVRITCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDR 201
|||||
Db 1 SSELTDPAVSVALGQTVRITCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDR 60
|||||

QY 202 FSGSSSGNTASLTITGAQAEDEADYVNSRDSSGNHVVFGGKLTVL 249
|||||
Db 61 FSGSSSGNTASLTITGAQAEDEADYVNSRDSSGNHVVFGGKLTVL 108
|||||

RESULT 7
D33548
Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression
A:Reference number: A33548; MUID:89345575
A:Accession: D33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.2%; Score 561; DB 2; Length 123;
Best Local Similarity 82.7%; Pred. No. 3.6e-33;
Matches 105; Conservative 8; Mismatches 10; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:|||||
Db 1 QVQLVQSGAEVKKPGASVKVSCEASGYTFTGHYMHVVRQAPGQGLEWMGWINPNSGGTNY 60
|||||

QY 61 AQKFGQGRVTMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
:|||||
Db 61 AEKFGQGRVTITRDTSTINTAYMELSLRLSRDSDTAVYYCARASYCGYDCY----YFFDYWGQG 116
|||||

QY 121 TLVTVSS 127
|||||
Db 117 TLVTVSS 123
|||||

RESULT 8
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries
A:Reference number: S36256; MUID:93178448
A:Accession: S36265
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GRI>
A:Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.2%; Score 547.5; DB 2; Length 118;
Best Local Similarity 81.9%; Pred. No. 3.1e-32;
Matches 104; Conservative 6; Mismatches 8; Indels 9; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:|||||
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPNSGGTNY 60
|||||

QY 61 AQKFGQGRVTMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
:|||||
Db 61 AQKFGQGRVTITRDTSTASTAYMELSLRLSRDSDTAVYYCARDFLSG-----YLDYWGQG 111
|||||

QY 121 TLVTVSS 127
|||||
Db 112 TLVTVSS 118
|||||

RESULT 9
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 546.5; DB 2; Length 135;
Best Local Similarity 83.5%; Pred. No. 4.2e-32;
Matches 106; Conservative 5; Mismatches 5; Indels 11; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:|||||
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPNSGGTNY 79
|||||

QY 61 AQKFGQGRVTMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
:|||||
Db 80 AQKFGQGRVTMTTRDTSISTAYMELSLRLSRDSDTAVYYCARAR---TG-----NYWGQG 128
|||||

QY 121 TLVTVSS 127
|||||
Db 129 TLVTVSS 135
|||||

RESULT 10
S70444
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: S70444; S70426

R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A;Reference number: S70442; MUID:93024508
A;Accession: S70444
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-127 <CUI>
A;Experimental source: clone E29.1
R;Tonnelle, C.
submitted to the EMBL Data Library, May 1990
A;Reference number: S70426
A;Accession: S70426
A;Molecule type: mRNA
A;Residues: 1-90 <TON>
A;Cross-references: EMBL:X53070
A;Experimental source: cell line E29.1, clone VL 29-1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 546; DB 2; Length 127;
Best Local Similarity 97.2%; Pred. No. 4.3e-32;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 142 SSELTPDPVSVVALGQTVRITCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDR 201
|||||
Db 20 SSELTPDPVSVVALGQTVRITCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDR 79
|||||

QY 202 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVYVFGGTKLTVL 249
|||||
Db 80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVYVFGTGTCTVTL 127
|||||

RESULT 11
S36272
Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36272
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448
A;Accession: S36272
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-110 <GRI>
A;Cross-references: EMBL:21833; NID:g33419; PIDN:CAA79285.1; PID:g939912
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 41.0%; Score 545.5; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 4e-32;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 142 SSELTPDPVSVVALGQTVRITCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDR 201
|||||
Db 1 SSELTPDPVSVVALGQTVRITCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDR 60
|||||

QY 202 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN-HVYVFGGTKLTVL 249
|||||
Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNLYVYVFGGTKLTVL 109
|||||

RESULT 12
S38498
Ig lambda chain - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from
A;Reference number: S38488
A;Accession: S38498
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <MAR>
A;Cross-references: EMBL:223035; NID:g414043; PIDN:CAA80570.1; PID:g414044
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>

Query Match 40.3%; Score 535; DB 2; Length 108;
Best Local Similarity 97.2%; Pred. No. 2.2e-31;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 143 SELTQDPVSVVALGQTVRITCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDRF 202
|||||
Db 1 SELTQDPVSVVALGQTVRITCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
|||||

QY 203 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVYVFGGTKLTVL 249
|||||
Db 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNWVFGGTKLTVL 107
|||||

RESULT 13
S38496
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38496
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from
A;Reference number: S38488
A;Accession: S38496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <MAR>
A;Cross-references: EMBL:223031; NID:g414039; PIDN:CAA80566.1; PID:g414040
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 533; DB 2; Length 109;
Best Local Similarity 93.5%; Pred. No. 3.1e-31;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 142 SSELTPDPVSVVALGQTVRITCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDR 201
|||||
Db 1 SSELTPDPVSVVALGQTVRITCQDLSKSYASWYQKPGQAPVLVYGNRPSGIPDR 60
|||||

QY 202 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVYVFGGTKLTVL 249
|||||
Db 61 FSGSYPGNTASLTITGAQAEDEADYYCTSRDTSNGNHLVFGGTKLTVL 108
|||||

RESULT 14
S23623
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S23623
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
A;Reference number: S23623; MUID:92156804

A:Accession: S23623
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <OLE>
A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 531; DB 2; Length 171;
Best Local Similarity 68.8%; Pred. No. 6.8e-31;
Matches 106; Conservative 12; Mismatches 24; Indels 12; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGTFYFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLVQSGAEVKKPGASVKVSCKGSGYFTFTAYQMHWVRQAPGQGLEWMGWINPNSGGTGY 79

QY 61 AOKFQGRVTMRDTSIGTAYMELSRSLSDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 GQKFGQGRVTLRDTSISTAYMELSRSLSDTAVYYCAIEFYDGSDL-KPSDVFIDWGQG 138

QY 121 TLVTVSSGGGGTGG-----GGSGGGGSSEL 145
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 139 TMVTVSS--ASTKGPSVFPLAPSSKSTSGGTAAL 170

RESULT 15
S25748
Ig lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25748
R:Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162
A:Accession: S25748
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 524; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 2.9e-30;
Matches 99; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 142 SSELTDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDR 201
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 SSELTDPAVSVALGQTVRITCOGDSLSRAYASWYQKPGQAPILVIYGNRRPSGIPDR 79

QY 202 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKLTVL 249
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 FSGSSSGNTASFAITGAQAEADYYCNSRDSSGDQVLFGGGKLTVL 127

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:21:20 ; Search time 410.32 Seconds
(without alignments)
999.360 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEFIYVIT.....QTCSTQTHKIMENKMCDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1:	/cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2:	/cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3:	/cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4:	/cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5:	/cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6:	/cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7:	/cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8:	/cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9:	/cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10:	/cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11:	/cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12:	/cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13:	/cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14:	/cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15:	/cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16:	/cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17:	/cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18:	/cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19:	/cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20:	/cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21:	/cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22:	/cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23:	/cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24:	/cgn2_6/ptodata/2/paa/US100_COMB.pep.*
25:	/cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26:	/cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6254	100.0	1165	9	US-08-570-142D-4
2	6254	100.0	1165	9	US-08-583-153A-4
3	6254	100.0	1165	9	US-08-585-005-2
4	6254	100.0	1165	10	US-08-638-524B-4
5	6254	100.0	1165	10	US-08-667-197-2
6	6254	100.0	1165	11	US-08-708-123D-4
7	6254	100.0	1165	11	US-08-779-457-2

8	6254	100.0	1165	11	US-08-780-562-2	Sequence 2, Appli
9	6254	100.0	1165	14	US-09-094-410-4	Sequence 4, Appli
10	6254	100.0	1165	15	US-09-137-132-4	Sequence 4, Appli
11	6254	100.0	1165	23	US-09-950-149-4	Sequence 4, Appli
12	6254	100.0	1216	11	US-08-774-414-7	Sequence 7, Appli
13	6254	100.0	1216	20	US-09-671-049-7	Sequence 7, Appli
14	6247	99.9	1167	23	US-09-948-933-284	Sequence 284, App
15	6247	99.9	1167	23	US-09-948-947-87	Sequence 87, Appl
16	6246	99.9	1165	9	US-08-599-974C-56	Sequence 56, Appl
17	6246	99.9	1165	11	US-08-713-296-11	Sequence 11, Appl
18	6246	99.9	1165	13	US-08-961-809-4	Sequence 4, Appli
19	6246	99.9	1165	15	US-09-178-691-4	Sequence 4, Appli
20	6246	99.9	1165	21	US-09-700-813-10	Sequence 10, Appl
21	6246	99.9	1165	23	US-09-948-933-256	Sequence 256, App
22	6246	99.9	1165	23	US-09-948-947-73	Sequence 73, Appl
23	6246	99.9	1165	24	US-10-095-929-11	Sequence 11, Appl
24	6240	99.8	1165	9	US-08-583-153-4	Sequence 4, Appli
25	6240	99.8	1165	9	US-08-599-455A-4	Sequence 4, Appli
26	6240	99.8	1165	10	US-08-638-524A-4	Sequence 4, Appli
27	6240	99.8	1165	11	US-08-708-123C-4	Sequence 4, Appli
28	6240	99.8	1165	12	US-08-864-564A-4	Sequence 4, Appli
29	6240	99.8	1165	24	US-10-079-625-4	Sequence 4, Appli
30	6236	99.7	1165	9	US-08-570-142B-4	Sequence 4, Appli
31	6236	99.7	1165	9	US-08-570-142C-4	Sequence 4, Appli
32	6172	98.7	1165	9	US-08-589-915A-11	Sequence 11, Appl
33	6032	96.5	1137	9	US-08-569-485-4	Sequence 4, Appli
34	5809	92.9	1221	13	US-08-982-430-2	Sequence 2, Appli
35	4831.5	77.3	969	9	US-08-582-825-5	Sequence 5, Appli
36	4831.5	77.3	969	9	US-08-582-825A-5	Sequence 5, Appli
37	4831.5	77.3	969	11	US-08-774-414-5	Sequence 5, Appli
38	4831.5	77.3	969	11	US-08-774-414-6	Sequence 6, Appli
39	4831.5	77.3	969	20	US-09-671-049-5	Sequence 5, Appli
40	4831.5	77.3	969	20	US-09-671-049-6	Sequence 6, Appli
41	4826	77.2	896	9	US-08-582-825-1	Sequence 1, Appli
42	4826	77.2	896	9	US-08-582-825A-1	Sequence 1, Appli
43	4826	77.2	896	9	US-08-585-005-3	Sequence 3, Appli
44	4826	77.2	896	10	US-08-667-197-3	Sequence 3, Appli
45	4826	77.2	896	11	US-08-779-457-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-570-142D-4
; Sequence 4, Application US/08570142D
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,142D
; FILING DATE: 11-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622

; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-570-142D-4

Query Match 100.0%; Score 6254; DB 9; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWFKLSKMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWFKLSKMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQWLKGDGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQWLKGDGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPEVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECECLVPVPTAKLNDTLMLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECECLVPVPTAKLNDTLMLKITSGGVIFQSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPPEPLQYQVYKYSNSTTVIREADKIVSATSLIVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPPEPLQYQVYKYSNSTTVIREADKIVSATSLIVDSILP 300
QY 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSEFHCYKKENKI 360
Db 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSEFHCYKKENKI 360
QY 361 VPSKEIYVWMMNLAEKIPQSQYDVVDVSDHVSQVTEFFNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWMMNLAEKIPQSQYDVVDVSDHVSQVTEFFNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAELYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAELYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYLOSDFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDLSQSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDLSQSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANENLTFSWPMKVNIVQSLAYSAPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 721 GASVANENLTFSWPMKVNIVQSLAYSAPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
QY 781 GEIKWLRISSSVKYYIHDHFIEPIEKYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFIEPIEKYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFKPETFEHLFI 900
Db 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFKPETFEHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEAEGETEYDEESQRPQFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETEYDEESQRPQFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFILLSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFNSSSWEIEAQAFILLSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLDSCSHFVENNINLTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLDSCSHFVENNINLTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
RESULT 2
US-08-583-153A-4
; Sequence 4, Application US/08583153A
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153A
; FILING DATE: 28-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/016001
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-583-153A-4

Query Match      100.0%; Score 6254; DB 9; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60

QY 61 NGHYTEAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYTEAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QQIDANNIQCWLKGLDKLFICYVESLFKLNFRNRYNYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 QQIDANNIQCWLKGLDKLFICYVESLFKLNFRNRYNYKVHLLYVLPEVLEDSPLVPQKGS 180

QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMVQPINMVKPDPP 240

QY 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVYKSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVYKSENSTTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEYQVRGKRLDGPGIWSDWSTPRVTTQDVYFPPPKILTSVGSNVSFHCYKKENKI 360
Db 301 GSSYEYQVRGKRLDGPGIWSDWSTPRVTTQDVYFPPPKILTSVGSNVSFHCYKKENKI 360

QY 361 VPSKEIVWMNLAEKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAELYVIDVNINISCESTDGYLTQKTCRWSTSTIQSLAESTLQIRYHRSSLYCSDIPSII 480
Db 421 RYAELYVIDVNINISCESTDGYLTQKTCRWSTSTIQSLAESTLQIRYHRSSLYCSDIPSII 480

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIIRYGLSGKEVQWKMYEYIDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIIRYGLSGKEVQWKMYEYIDAKSKSVSLPV 600

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWEVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWEVDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSPDKLMYFIEWKNLNED 780
Db 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSPDKLMYFIEWKNLNED 780

QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
```

```

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQLNFQKPFTEHLEFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQLNFQKPFTEHLEFI 900

QY 901 KHTASVTCGPPLLLEPETISEDISVDTSWKNKDEMMPPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPPLLLEPETISEDISVDTSWKNKDEMMPPTTVVSLSTTDLEKGSVCISDQFN 960

QY 961 SYNFESEABGTEVTYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNNSPL 1020
Db 961 SYNFESEABGTEVTYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNNSPL 1020

QY 1021 KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSGLDELKLEGNFPEENNDKKSIIYYL 1080
Db 1021 KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSGLDELKLEGNFPEENNDKKSIIYYL 1080

QY 1081 GVTSIKKRESGVLLTDKSRVSCPPFPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPFPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS 1140

QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

RESULT 3
US-08-585-005-2
; Sequence 2, Application US/08585005
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585.005
; FILING DATE: 08-Jan-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-585-005-2
```

```

Query Match      100.0%; Score 6254; DB 9; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
```

QY 61 NGHETAVEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPEVLEDSPLVPQKGS 180
QY 181 FQMVHCNSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FQMVHCNSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSPPPLVPFPPLQYQVKYSENSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSPPPLVPFPPLQYQVKYSENSTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGKRLDGGIWSDWSTPRVFTTQDVYPPPKILTSVGSNVSFHCYKKENKI 360
Db 301 GSSYEVQVRGKRLDGGIWSDWSTPRVFTTQDVYPPPKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIYVWMNLAEKIPQSYDVSVDHVSKVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWMNLAEKIPQSYDVSVDHVSKVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAELYVIDVNNINISCEYDGYLTMTKTCRWSTSTIQSLAESTLQLRHYRSSLYCSDIPSII 480
Db 421 RYAELYVIDVNNINISCEYDGYLTMTKTCRWSTSTIQSLAESTLQLRHYRSSLYCSDIPSII 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVDYDAKSVSILPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVDYDAKSVSILPV 600
QY 601 PDLCAVYAVQVRCRKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSYEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSYEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFLTFSWPMKSNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKKNLNE 780
Db 721 GASVANFLTFSWPMKSNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKKNLNE 780
QY 781 GEIKWLRISSSVKKYIYIHDHFPIPIEKYQFSLYPIFMEGVGKPKIINSETQDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIYIHDHFPIPIEKYQFSLYPIFMEGVGKPKIINSETQDIEKHQSDA 840
QY 841 GLYVIVPVIISSSILLGTLTLLSHQRMKKLFWDVVPNPKNCVWAQGLNFOKPFTEHFLFI 900
Db 841 GLYVIVPVIISSSILLGTLTLLSHQRMKKLFWDVVPNPKNCVWAQGLNFOKPFTEHFLFI 900
QY 901 KHTASVTCGPILLLEPETISEDIVSDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPILLLEPETISEDIVSDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEAEGETEVTYEDESQRPVVKYATLISNPKPSETGEEQGLINSSVTKCFSSKN SPL 1020
Db 961 SVNFSEAEGETEVTYEDESQRPVVKYATLISNPKPSETGEEQGLINSSVTKCFSSKN SPL 1020
QY 1021 KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSGLDELKLEGNFPERNDKKSIYYL 1080
Db 1021 KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSGLDELKLEGNFPERNDKKSIYYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
RESULT 4
US-08-638-524B-4
; Sequence 4, Application US/08638524B
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,524B
; FILING DATE: 26-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-638-524B-4

Query Match 100.0%; Score 6254; DB 10; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKNLFRNRYNKKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKNLFRNRYNKKVHLLYVLPEVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLIWSDDWSTPRVFTTQDVIFPPPKILT SVGSNVSFHCIIYKKNKI 360
Db 301 GSSYEYQVRGKRLDGPGLIWSDDWSTPRVFTTQDVIFPPPKILT SVGSNVSFHCIIYKKNKI 360
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFEFLNLTETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFEFLNLTETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCEYDGLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSII 480
Db 421 RYAEIYVIDVNIINISCEYDGLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSII 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRNHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRNHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEYDVGNIHKTFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEYDVGNIHKTFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIIEWKNLNE 780
Db 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIIEWKNLNE 780
QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYQFSLYPIPMGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSVKKYYIHDHFIPIEKYQFSLYPIPMGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPEFHLFI 900
Db 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPEFHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSAEAGTEVTYEDESOROPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSAEAGTEVTYEDESOROPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKSIYYL 1080
Db 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKSIYYL 1080
QY 1081 GVTISIKKRESGVLITDKSRVSCFPAPACFLTDIRVLQDSCSHFVENNINLTSSSKKTFAS 1140
Db 1081 GVTISIKKRESGVLITDKSRVSCFPAPACFLTDIRVLQDSCSHFVENNINLTSSSKKTFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 5
US-08-667-197-2
; Sequence 2, Application US/08667197 '
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,197
; FILING DATE: 20-Jun-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0986P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-667-197-2

Query Match 100.0%; Score 6254; DB 10; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNNTS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNNTS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKNLFRNRYNKKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKNLFRNRYNKKVHLLYVLPEVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLIWSDDWSTPRVFTTQDVIFPPPKILT SVGSNVSFHCIIYKKNKI 360
Db 301 GSSYEYQVRGKRLDGPGLIWSDDWSTPRVFTTQDVIFPPPKILT SVGSNVSFHCIIYKKNKI 360
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFEFLNLTETKPRGKFTYDAVYCCNEHECHH 420


```
Db 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RYAELYVIDVNNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRHYRSSLYCS DIPSIH 480
Db 421 RYAELYVIDVNNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRHYRSSLYCS DIPSIH 480
Qy 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLFQFIIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQFIIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Qy 601 PDLCAVYAVQVRCRRLDGLGYNSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRRLDGLGYNSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Qy 661 TLLWKLPMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKLPMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Qy 721 GASVANFNLTFSWPMKSVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Qy 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTQDDIEKHQSDA 840
Qy 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCWAQGLNFQKPETFEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCWAQGLNFQKPETFEHLFI 900
Qy 901 KHTASVTCGPLLLEPETISEDIVSDTSWKNKDEMPTTVVSVLLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDIVSDTSWKNKDEMPTTVVSVLLSTTDLEKGSVCISDQFN 960
Qy 961 SVNFSEAEGETVTEYDESRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETVTEYDESRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Qy 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Qy 1081 GVTSIKKRESGVLLTDKSRVSCPPFPAPCLFTDIRVLQDSCSHFVENNINLTGTSKKTFPAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPFPAPCLFTDIRVLQDSCSHFVENNINLTGTSKKTFPAS 1140
Qy 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

RESULT 6
US-08-708-123D-4
; Sequence 4, Application US/08708123D
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
```

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; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/708,123D
; FILING DATE: 03-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-708-123D-4
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Query Match 100.0%; Score 6254; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTDYFLLPAGLSKNTSNS 60
Qy 61 NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Qy 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Qy 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Qy 241 LGLHMEITDDGNLKISWSSPPLVPFPFLOQYQVKYSENSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPFLOQYQVKYSENSTVIREADKIVSATSLLVDSILP 300
Qy 301 GSSYEYQVVRGKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI 360
Db 301 GSSYEYQVVRGKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI 360
Qy 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
```

QY 421 RYAEALYVIDVNNINISCETDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAEALYVIDVNNINISCETDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYLQSDGFYECIFQIFILLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQIFILLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYSNWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYSNWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIIIEWKNLNE 780
Db 721 GASVANFNLTFSWPMKSVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIIIEWKNLNE 780
QY 781 GEIKWLRISSSVKKYIHDHFTPIEKYQFSLPIFMEGVCKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIHDHFTPIEKYQFSLPIFMEGVCKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVIISSILLGLTLISHQRMKKLFWEDVPNPKNCWSAQGLNFQKPTFEHLFI 900
Db 841 GLYVIVPVIISSILLGLTLISHQRMKKLFWEDVPNPKNCWSAQGLNFQKPTFEHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDIVSDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDIVSDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSRAEGTEVYDESORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSRAEGTEVYDESORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPEENNDKKSIIYL 1080
Db 1021 KDSFSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPEENNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTGSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTGSSKKTFFAS 1140
QY 1141 YMQPOTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMQPOTCSTQTHKIMENKMCDLTV 1165

RESULT 7
US-08-779-457-2
; Sequence 2, Application US/08779457
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-779-457-2

Query Match 100.0%; Score 6254; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNTS 60
Qy 61 NGHETAVEPKFNSSGTHFNSLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKFNSSGTHFNSLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Qy 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYNKVHLLVYLVPEVLEDSPLVPQKS 180
Db 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYNKVHLLVYLVPEVLEDSPLVPQKS 180
Qy 181 FQVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDPP 240
Db 181 FQVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDPP 240
Qy 241 LGLHWEITDDGNLKIWSSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLDVDSILP 300
Db 241 LGLHWEITDDGNLKIWSSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLDVDSILP 300
Qy 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
Qy 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RYAEALYVIDVNNINISCETDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAEALYVIDVNNINISCETDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Qy 481 PISEPKDCYLQSDGFYECIFQIFILLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQIFILLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600

QY 601 PDLCAVAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTSESDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTSESDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSETQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSETQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVVPNPKNCSWAOGNLFQKPFTEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVVPNPKNCSWAOGNLFQKPFTEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDOFN 960
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDOFN 960
QY 961 SVNFSEAEGETVYEDESQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETVYEDESQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSGLDELLKLEGNEPENNNDKKSIIYL 1080
Db 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSGLDELLKLEGNEPENNNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

RESULT 8

US-08-780-562-2
; Sequence 2, Application US/08780562
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/
; FILING DATE: 01/08/97
; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-780-562-2

Query Match 100.0%; Score 6254; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPKFNSSGTHFSNLSKTTTCHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKFNSSGTHFSNLSKTTTCHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQWLKGDLLKLFICYVESLEFKNLFRNRYNYKVHLLYVLPVELEDSPVPQKGS 180
Db 121 QQIDANWNIQWLKGDLLKLFICYVESLEFKNLFRNRYNYKVHLLYVLPVELEDSPVPQKGS 180
QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDGNLKIWSWSPPLVPFPLOYQVKYSENSTTVIREADKIYVATSLLVDSILP 300
Db 241 LGLHMEITDGNLKIWSWSPPLVPFPLOYQVKYSENSTTVIREADKIYVATSLLVDSILP 300
QY 301 GSSYEVOVRGKRLDGPGLWSDWSTPRVFTQDVYIFPPKILTSVGSNVSFHICYKKNKI 360
Db 301 GSSYEVOVRGKRLDGPGLWSDWSTPRVFTQDVYIFPPKILTSVGSNVSFHICYKKNKI 360
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSVKVTFEENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSVKVTFEENLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAELYVIDVNIINISCEETDGYLTMTCKRSTSTIQSLAESTLQLRHYRSSLYCSIDPSIH 480
Db 421 RYAELYVIDVNIINISCEETDGYLTMTCKRSTSTIQSLAESTLQLRHYRSSLYCSIDPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLPQIRYGLSGKEVQWKMYEVDKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKVPFPENNLPQIRYGLSGKEVQWKMYEVDKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTSESDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTSESDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSETQDDIEKHQSDA 840

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Db 781 GEIKWLRISSVKKYYIHDHFIEPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLISHQRMKKLFWEDVPNPKNCSWAOGLNFKQKPEFHLFI 900
Db 841 GLYVIVPVISSSILLGLTLISHQRMKKLFWEDVPNPKNCSWAOGLNFKQKPEFHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPITVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPITVVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEAECTEVTYEDESQRPVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAECTEVTYEDESQRPVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGDLLEKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGDLLEKLEGNFPEENNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

RESULT 9
US-09-094-410-4
; Sequence 4, Application US/09094410
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,410
; FILING DATE: 09-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
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; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-094-410-4
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Query Match 100.0%; Score 6254; DB 14; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVWLLHWEFIYVITAFNLSPITPWRFKLSCLMPNPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVWLLHWEFIYVITAFNLSPITPWRFKLSCLMPNPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPKFNSSGTHFNSLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKFNSSGTHFNSLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGDCLKFTCYVESLFKNLFRNRYKVHLLYVLPVELEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGDCLKFTCYVESLFKNLFRNRYKVHLLYVLPVELEDSPLVPQKGS 180
QY 181 FOMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FOMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEYQVRGKRLDGGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKENKI 360
Db 301 GSSYEYQVRGKRLDGGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTAKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTAKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLFQFIYRGLSGKEVQWKMYEVDKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKVPFPENNLFQFIYRGLSGKEVQWKMYEVDKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSQVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSQVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMSKVNIVQSLISAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
Db 721 GASVANFNLTFSWPMSKVNIVQSLISAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
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QY 781 GEIKWLRISSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
    |||||||
Db 781 GEIKWLRISSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
    |||||||
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPFTEHLFI 900
    |||||||
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPFTEHLFI 900
    |||||||
QY 901 KHTASVTCGPILEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
    |||||||
Db 901 KHTASVTCGPILEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
    |||||||
QY 961 SVNFSEAEGETVYIYEDESQRPQFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
    |||||||
Db 961 SVNFSEAEGETVYIYEDESQRPQFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
    |||||||
QY 1021 KDSFSNSSWEIAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNPEENNNDKKSIIYL 1080
    |||||||
Db 1021 KDSFSNSSWEIAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNPEENNNDKKSIIYL 1080
    |||||||
QY 1081 GVTSIKKRESGVLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS 1140
    |||||||
Db 1081 GVTSIKKRESGVLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS 1140
    |||||||
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
    |||||||
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
    |||||||

RESULT 10
US-09-137-132-4
; Sequence 4, Application US/09137132
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
```

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; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-137-132-4

Query Match 100.0%; Score 6254; DB 15; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSMPPNSTDYFLLPAGLSKNTSNS 60
    |||||||
Db 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSMPPNSTDYFLLPAGLSKNTSNS 60
    |||||||
QY 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVP 120
    |||||||
Db 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVP 120
    |||||||
QY 121 QQIDANWNIQCWLKGDCLKFICYVESLFKNLFRNRYKVHLLYVLPEVLEDSPLVPQKGS 180
    |||||||
Db 121 QQIDANWNIQCWLKGDCLKFICYVESLFKNLFRNRYKVHLLYVLPEVLEDSPLVPQKGS 180
    |||||||
QY 181 FQMVHCNSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
    |||||||
Db 181 FQMVHCNSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
    |||||||
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
    |||||||
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
    |||||||
QY 301 GSSYEVQVRGKRDLGPGIWSDDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI 360
    |||||||
Db 301 GSSYEVQVRGKRDLGPGIWSDDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI 360
    |||||||
QY 361 VPSKEIYVWMNLAEKIPQSQYDVVDVSHVSKVTFPNLNETKPRGKETDYAVYCCNEHECHH 420
    |||||||
Db 361 VPSKEIYVWMNLAEKIPQSQYDVVDVSHVSKVTFPNLNETKPRGKETDYAVYCCNEHECHH 420
    |||||||
QY 421 RYAELYVIDVNNINISCE TDGYLT KMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPS IH 480
    |||||||
Db 421 RYAELYVIDVNNINISCE TDGYLT KMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPS IH 480
    |||||||
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVWKPLPP 540
    |||||||
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVWKPLPP 540
    |||||||
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
    |||||||
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
    |||||||
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPPEFWRILNGDTMKKEKNV 660
    |||||||
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPPEFWRILNGDTMKKEKNV 660
    |||||||
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSQVGNHTKFTFLWTEQAHTVTVLAINSI 720
    |||||||
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSQVGNHTKFTFLWTEQAHTVTVLAINSI 720
    |||||||
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QY 721 GASVANFNLTSPWPMKSVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMVFIEWKNLNED 780
Db 721 GASVANFNLTSPWPMKSVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMVFIEWKNLNED 780
QY 781 GEIKWLRISSSVKKYYIHDHFIFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWDVVPNPKNCSWAQLNFQKPEFHEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWDVVPNPKNCSWAQLNFQKPEFHEHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPPTTVVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEAEGETVYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETVYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNPEENNDKKSIIYL 1080
Db 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNPEENNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLTLTKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLTLTKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

RESULT 11
US-09-950-149-4
; Sequence 4, Application US/09950149
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; Tepper, Robert I.
; Culpepper, Janice A.
; White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fastseq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/950,149
; FILING DATE: 10-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,781
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995

; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-950-149-4

Query Match 100.0%; Score 6254; DB 23; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWFKLSKMPNSTYDYFLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWFKLSKMPNSTYDYFLPAGLSKNTS 60
QY 61 NGHYETAPEKFNSSGTHFNSLSKTTFHCCFSEQRNCSLCAADNIEGKTFVSTVNSLV 120
Db 61 NGHYETAPEKFNSSGTHFNSLSKTTFHCCFSEQRNCSLCAADNIEGKTFVSTVNSLV 120
QY 121 QQIDANWNIQCWLKGLDLKLFICYVESLFKNLFRNRYKVHLLYVLPEVLEDSPLVPQKS 180
Db 121 QQIDANWNIQCWLKGLDLKLFICYVESLFKNLFRNRYKVHLLYVLPEVLEDSPLVPQKS 180
QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLMLKITSGGVIFQSPLMSVQPINVMKPDPP 240
Db 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLMLKITSGGVIFQSPLMSVQPINVMKPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVYKSENSTTVIREADKIVSATSLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVYKSENSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVQVRGKRLDGPGLSDWSTPRVFTTQDVIYFPPKILTSVGSNVSPHICYKKENKI 360
Db 301 GSSYEVQVRGKRLDGPGLSDWSTPRVFTTQDVIYFPPKILTSVGSNVSPHICYKKENKI 360
QY 361 VPSKEIVWMNLAKIPQSQYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAKIPQSQYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPS 480
Db 421 RYAEIYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPS 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLQFIQRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLQFIQRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDLSCSVORYVINHHHTSCNGTWSVDVGNHHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDLSCSVORYVINHHHTSCNGTWSVDVGNHHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
QY 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCVWAQGLNFQKPFTEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCVWAQGLNFQKPFTEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTDLEKGSVCISDQFN 960
QY 961 SVNFSEAGTEVTYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNNSPL 1020
Db 961 SVNFSEAGTEVTYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNNSPL 1020
QY 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPEENNDKKSIIYL 1080
Db 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPEENNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
RESULT 12
US-08-774-414-7
; Sequence 7, Application us/08774414
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: WELCHER, ANDREW A.
; APPLICANT: FLETCHER, FREDERICK A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1216 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-774-414-7
Query Match 100.0%; Score 6254; DB 11; Length 1216;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDP 240
Db 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKIWSWSSPPLVPFPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSWSSPPLVPFPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGKRLDGPGLWSWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIIYKKENKI 360
Db 301 GSSYEVQVRGKRLDGPGLWSWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIIYKKENKI 360
QY 361 VPSKEIYVWMNLAEKIPQSQYDVVSDHVSQVTFNINNETKPRGKFTYDAVYCNEHECHH 420
Db 361 VPSKEIYVWMNLAEKIPQSQYDVVSDHVSQVTFNINNETKPRGKFTYDAVYCNEHECHH 420
QY 421 RYAEIYVIDVINISCTDGYLTMTKTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPI 480
Db 421 RYAEIYVIDVINISCTDGYLTMTKTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPI 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRNHSIGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRNHSIGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOQFIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOQFIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDLSCSVORYVINHHHTSCNGTWSVDVGNHHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDLSCSVORYVINHHHTSCNGTWSVDVGNHHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
QY 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCVWAQGLNFQKPFTEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCVWAQGLNFQKPFTEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTDLEKGSVCISDQFN 960
QY 961 SVNFSEAGTEVTYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNNSPL 1020
Db 961 SVNFSEAGTEVTYEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNNSPL 1020

Db 961 SVNFSEAEGETVTEYDESRQPFVKYATLISNSKPSKSETGEEGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFILSDQHNPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFNSSSWEIEAQAFILSDQHNPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMCMLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCMLTV 1165

RESULT 13

US-09-671-049-7
; Sequence 7, Application US/09671049
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; WELCHER, ANDREW A.
; FLETCHER, FREDERICK A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/671,049
; FILING DATE: 27-Sep-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,414
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1216 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-671-049-7

Query Match 100.0%; Score 6254; DB 20; Length 1216;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEKFNSSGTHFSNLSKTTHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF 120
Db 61 NGHYETAPEKFNSSGTHFSNLSKTTHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQWLKGDLLKLFICYVESLFLKFNLYNYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQWLKGDLLKLFICYVESLFLKFNLYNYKVHLLYVLPEVLEDSPLVPQKGS 180

QY 181 FQVHCNCVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FQVHCNCVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGKRLDGPGLIWSWDSTPRVFTQDVIYFPPKILTSVGSNVSEFHCIIYKKENKI 360
Db 301 GSSYEVQVRGKRLDGPGLIWSWDSTPRVFTQDVIYFPPKILTSVGSNVSEFHCIIYKKENKI 360
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFFFNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFFFNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAELYVIDVNIINISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSIIH 480
Db 421 RYAELYVIDVNIINISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSIIH 480
QY 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHVTVLAINSI 720
QY 721 GASVANFLTFSWPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 721 GASVANFLTFSWPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
QY 781 GEIKWLRISSSVKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVIISILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQLNFKQKPFTEHFLFI 900
Db 841 GLYVIVPVIISILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQLNFKQKPFTEHFLFI 900
QY 901 KHTASVTCGPIILLEPETISEDISVDTSWKNKDEMMPTTVVSLSTTDLKSGVCISDQFN 960
Db 901 KHTASVTCGPIILLEPETISEDISVDTSWKNKDEMMPTTVVSLSTTDLKSGVCISDQFN 960
QY 961 SVNFSEAEGETVTEYDESRQPFVKYATLISNSKPSKSETGEEGLINSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETVTEYDESRQPFVKYATLISNSKPSKSETGEEGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFILSDQHNPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFNSSSWEIEAQAFILSDQHNPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMCMLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCMLTV 1165

RESULT 14
US-09-948-933-284
; Sequence 284, Application US/09948933
; GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Human
; US-09-948-933-284

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Query Match		99.9%;	Score 6247;	DB 23;	Length 1167;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1163;	Conservative	2;	Mismatches	0;	Indels
					Gaps
					0;
QY	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS	60		
DB	3	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS	62		
QY	61	NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120		
DB	63	NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF	122		
QY	121	QQIDANWNIQCWLKGLKLFICYVESLFKFNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS	180		
DB	123	QQIDANWNIQCWLKGLKLFICYVESLFKFNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS	182		
QY	181	FQMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMVKPDPP	240		
DB	183	FQMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSGVIFRSPMSVQPINMVKPDPP	242		
QY	241	LGLHMEITDGNLKISWSSPPLVPFPLOYQVKYSENSTVIREADKIVSATSLLVDSILP	300		
DB	243	LGLHMEITDGNLKISWSSPPLVPFPLOYQVKYSENSTVIREADKIVSATSLLVDSILP	302		
QY	301	GSSYEVOVGRKRLDGPISWSDWSTPRVFTTQDVYFPFKILTSGSNVSFHCYKKNKI	360		
DB	303	GSSYEVOVGRKRLDGPISWSDWSTPRVFTTQDVYFPFKILTSGSNVSFHCYKKNKI	362		
QY	361	VPSKEIYVWMNLAEKIPQSQYDVSDHVSKVTFNENLNETKPRGKFTYDAVYCCNEHECHH	420		
DB	363	VPSKEIYVWMNLAEKIPQSQYDVSDHVSKVTFNENLNETKPRGKFTYDAVYCCNEHECHH	422		
QY	421	RYAELYVIDVNINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPS IH	480		
DB	423	RYAELYVIDVNINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPS IH	482		
QY	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPP	540		
DB	483	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPP	542		
QY	541	SSVKAELITINIGLLKISWEKVPFPENNLFQIRYGLSKEVQWKMYEYDAKSVS LVP	600		
DB	543	SSVKAELITINIGLLKISWEKVPFPENNLFQIRYGLSKEVQWKMYEYDAKSVS LVP	602		
QY	601	PDLCAVAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660		
DB	603	PDLCAVAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	662		
QY	661	TLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSEDVGNHKTFTFLWTEQAHTVTVLAINSI	720		
DB	663	TLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSEDVGNHKTFTFLWTEQAHTVTVLAINSI	722		
QY	721	GASVANENLTFSPMSKVNIVQSLSAYPLNSSCVIYSWILSPSDYKLMYFII EWKNLNE D	780		
DB	723	GASVANENLTFSPMSKVNIVQSLSAYPLNSSCVIYSWILSPSDYKLMYFII EWKNLNE D	782		

QY	781	GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA	840
Db	783	GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA	842
QY	841	GLYVIVPVISSSILILGTILISHQRMKCLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI	900
Db	843	GLYVIVPVISSSILILGTILISHQRMKCLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI	902
QY	901	KHTASVTCGPLLEPETISEDISVDTSWKNKDEMMPPTVVYLLSTTDLEKGSVCISDQFN	960
Db	903	KHTASVTCGPLLEPETISEDISVDTSWKNKDEMMPPTVVYLLSTTDLEKGSVCISDQFN	962
QY	961	SVNFSEAEGETVYEDESQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL	1020
Db	963	SVNFSEAEGETVYEDESQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL	1022
QY	1021	KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL	1080
Db	1023	KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL	1082
QY	1081	GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS	1140
Db	1083	GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFAS	1142
QY	1141	YMPQFQTCSTQTHKIMENKMCDLTV	1165
Db	1143	YMPQFQTCSTQTHKIMENKMCDLTV	1167
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US-09-948-947-87			
; Sequence 87, Application US/09948947			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND			
; TITLE OF INVENTION: USES THEREOF			
; FILE REFERENCE: CL000786			
; CURRENT APPLICATION NUMBER: US/09/948,947			
; CURRENT FILING DATE: 2001-09-10			
; PRIOR APPLICATION NUMBER: 60/231,397			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 2172			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 87			
; LENGTH: 1167			
; TYPE: PRT			
; ORGANISM: Human			
US-09-948-947-87			

Query Match 99.9%; Score 6247; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 1163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	MICQKFCVVLHWEFIYVITAFNLSYPITPWRFKLSMPNPSTYDYFLLPAGLSKNTSNS	60
Db	3	MICQKFCVVLHWEFIYVITAFNLSYPITPWRFKLSMPNPSTYDYFLLPAGLSKNTSNS	62
QY	61	NGHYETAVERPENSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	63	NGHYETAVERPENSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF	122
QY	121	QQIDANNWNIQCWLKGDCLKFCYVESLFKNLFRNYYKVHLLYVLPVLEDSPLVPQKGS	180
Db	123	QQIDANNWNIQCWLKGDCLKFCYVESLFKNLFRNYYKVHLLYVLPVLEDSPLVPQKGS	182
QY	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPIMSVQPINMVKPDPP	240
Db	183	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPIMSVQPINMVKPDPP	242
QY	241	LGLHMEITDGNLKIWSSSPPLVPPLPQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300

Db 243 LGLHMEITDDGNLKISWSSPPLVPFPLOQVKYSENSTTVIREADKIVSATSLLVDSILP 302
QY 301 GSSYEYQVRGKRLDGPGIWSDNSTPRVFTTQDVYFPPKILTSVGSNVSFHCIIYKKENKI 360
Db 303 GSSYEYQVRGKRLDGPGIWSDNSTPRVFTTQDVYFPPKILTSVGSNVSFHCIIYKKENKI 362
QY 361 VPSKEIVWWMNLAEKIPQSQYDVVDHVSUKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIVWWMNLAEKIPQSQYDVVDHVSUKVTFNLTNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNNINISCETDGYLTMTKTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480
Db 423 RYAEIYVIDVNNINISCETDGYLTMTKTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSYEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 663 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSYEDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMSKVNIQSLSAYPLNSSCVIVSWILSPDYKLMYFIIWKKNLNE 780
Db 723 GASVANFNLTFSWPMSKVNIQSLSAYPLNSSCVIVSWILSPDYKLMYFIIWKKNLNE 782
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKKHQS 840
Db 783 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKKHQS 842
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPEFHEHFI 900
Db 843 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPEFHEHFI 902
QY 901 KHTASVTCGPLLLEPETISEDIVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 903 KHTASVTCGPLLLEPETISEDIVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 962
QY 961 SVNFSEAEGTEVTYEDSQRPQFVKYATLISNKPSETGEEGLINSSVTKCFSSKN SPL 1020
Db 963 SVNFSEAEGTEVTYEDSQRPQFVKYATLISNKPSETGEEGLINSSVTKCFSSKN SPL 1022
QY 1021 KDSFNSSSWEIEAQAFFILSDQHNPNIISPHLTFFSEGLDELLKLEGNFPEENNDKKSIIY 1080
Db 1023 KDSFNSSSWEIEAQAFFILSDQHNPNIISPHLTFFSEGLDELLKLEGNFPEENNDKKSIIY 1082
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS 1140
Db 1083 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS 1142
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1143 YMPQFQTCSTQTHKIMENKMCDLTV 1167

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:20:55 ; Search time 111.01 Seconds
(without alignments)
2425.061 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEFIYVIT.....QTCSTQTHKIMENKMCDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 698052 seqs, 231078099 residues

Total number of hits satisfying chosen parameters: 698052

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6254	100.0	1165	5	US-09-791-537-95040, A
2	6246	99.9	1165	5	US-09-791-537-120058, A
3	5967	95.4	1163	5	US-09-791-537-14096, A
4	5941.5	95.0	1194	5	US-09-791-537-75134, A
5	4831.5	77.3	958	5	US-09-791-537-95039, A
6	4826	77.2	896	5	US-09-791-537-95038, A
7	4819.5	77.1	958	5	US-09-791-537-114050, A
8	4816	77.0	896	5	US-09-791-537-114052, A
9	4814	77.0	896	5	US-09-791-537-114053, A
10	4786.5	76.5	1162	5	US-09-791-537-128089, A
11	4778.5	76.4	1162	5	US-09-791-537-57257, A
12	4766.5	76.2	1162	5	US-09-791-537-65061, A
13	4766.5	76.2	1174	5	US-09-791-537-26913, A
14	4761.5	76.1	1162	5	US-09-791-537-53431, A
15	4760.5	76.1	1162	5	US-09-791-537-45617, A
16	4757.5	76.1	1162	5	US-09-791-537-91206, A
17	4591	73.4	925	5	US-09-791-537-75138, A
18	4590	73.4	894	5	US-09-791-537-75131, A
19	3787	60.6	894	5	US-09-791-537-76191, A
20	3781	60.5	894	5	US-09-791-537-11623, A
21	3779	60.4	894	5	US-09-791-537-144499, A
22	3340	53.4	805	5	US-09-791-537-144103, A
23	3337	53.4	805	5	US-09-791-537-144369, A
24	2775	44.4	1148	5	US-09-791-537-8198, Ap
25	2693	43.1	1146	5	US-09-791-537-126327, A
26	1620	25.9	308	6	US-10-038-010-46, Appl

27	934	14.9	179	6	US-10-038-010-44	Sequence 44, Appl
28	703	11.2	133	6	US-10-038-010-42	Sequence 42, Appl
29	444	7.1	881	5	US-09-791-537-142984	Sequence 142984, A
30	409.5	6.5	918	5	US-09-791-537-56948	Sequence 56948, A
31	384	6.1	1158	5	US-09-935-868-26	Sequence 26, Appl
32	376	6.0	1168	5	US-09-935-868-24	Sequence 24, Appl
33	354	5.7	710	5	US-09-791-537-143846	Sequence 143846, A
34	345.5	5.5	918	1	PCT-US02-19669-230	Sequence 230, App
35	345.5	5.5	918	5	US-09-853-180-4	Sequence 4, Appli
36	345.5	5.5	918	5	US-09-829-472A-9	Sequence 9, Appli
37	345.5	5.5	918	5	US-09-791-537-118267	Sequence 118267, A
38	345.5	5.5	918	6	US-10-177-293-230	Sequence 230, App
39	313	5.0	837	5	US-09-791-537-99945	Sequence 99945, A
40	309.5	4.9	859	5	US-09-935-868-7	Sequence 7, Appli
41	308.5	4.9	951	5	US-09-935-868-9	Sequence 9, Appli
42	295.5	4.7	1078	5	US-09-791-537-21626	Sequence 21626, A
43	294.5	4.7	1097	5	US-09-791-537-120086	Sequence 120086, A
44	288.5	4.6	863	5	US-09-791-537-5078	Sequence 5078, Ap
45	284	4.5	783	5	US-09-791-537-78448	Sequence 78448, A

ALIGNMENTS

RESULT 1
US-09-791-537-95040
; Sequence 95040, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95040
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-95040

Query Match	100.0%;	Score 6254;	DB 5;	Length 1165;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1165;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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Db	1	MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNS	60	
Qy	61	NGHYETAVERKFNSSGTHFSNLSTKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120	
Db	61	NGHYETAVERKFNSSGTHFSNLSTKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120	
Qy	121	QQIDANWNIQCWLKGDLLKLFICYVESLFKNLFRNRYNKKVHLLYVLPVELEDSPLVPQKGS	180	
Db	121	QQIDANWNIQCWLKGDLLKLFICYVESLFKNLFRNRYNKKVHLLYVLPVELEDSPLVPQKGS	180	
Qy	181	FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMKVDPDP	240	
Db	181	FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMKVDPDP	240	
Qy	241	LGLHMEITDGNLKISWSSPPLVPFPLOYVKYSENSTTVIREADKIVSATSLLVDSILP	300	
Db	241	LGLHMEITDGNLKISWSSPPLVPFPLOYVKYSENSTTVIREADKIVSATSLLVDSILP	300	
Qy	301	GSSYEVOVRGKRLDGPISWDWSTPRVFTTQDVIYFPFKILTSGVNSVSHCIYKKENKI	360	
Db	301	GSSYEVOVRGKRLDGPISWDWSTPRVFTTQDVIYFPFKILTSGVNSVSHCIYKKENKI	360	

QY 361 VPSKEIIVWMNLAEKIPQSQYDVVSDHVSQVTFNQLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIIVWMNLAEKIPQSQYDVVSDHVSQVTFNQLNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAELYVIDVNNINISCTDGYLTMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSII 480
Db 421 RYAELYVIDVNNINISCTDGYLTMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSII 480

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSQSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSQSVSLPV 600

QY 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSHEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSHEDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKSNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780

QY 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPFTEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPFTEHLFI 900

QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTTDLEKGSVCISDQFN 960

QY 961 SVNFSEAEGETVYEDESQRPVVKYATLISNKPSETGEEQGLINSSVTCKFSSKNSPL 1020
Db 961 SVNFSEAEGETVYEDESQRPVVKYATLISNKPSETGEEQGLINSSVTCKFSSKNSPL 1020

QY 1021 KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSGLDELLKLEGFPENNDDKKSIIYL 1080
Db 1021 KDSFSNSSWEIEAQAFILSDQHPNIIISPHLTFSGLDELLKLEGFPENNDDKKSIIYL 1080

QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGSKKTFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGSKKTFAS 1140

QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

RESULT 2
US-09-791-537-120058
; Sequence 120058, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 120058
; LENGTH: 1165

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-120058

Query Match 99.9%; Score 6246; DB 5; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPIITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPIITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60

QY 61 NGHYETAPEKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAPEKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QQIDANWNIQCWLKGDULKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGDULKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS 180

QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINMVKPDPP 240

QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEVQVRGKRLDGPGLIWSDWSTPRVFTTQDVIYFPPKILTSVGSNSVSHFCIYKKENKI 360
Db 301 GSSYEVQVRGKRLDGPGLIWSDWSTPRVFTTQDVIYFPPKILTSVGSNSVSHFCIYKKENKI 360

QY 361 VPSKEIIVWMNLAEKIPQSQYDVVSDHVSQVTFNQLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIIVWMNLAEKIPQSQYDVVSDHVSQVTFNQLNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAELYVIDVNNINISCTDGYLTMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSII 480
Db 421 RYAELYVIDVNNINISCTDGYLTMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSII 480

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSQSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYDAKSQSVSLPV 600

QY 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSHEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSHEDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKSNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780

QY 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPFTEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPFTEHLFI 900

QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLSTTDLEKGSVCISDQFN 960

QY	961	SVNFSEAE	GVTE	YED	ESQR	QPFV	KYAT	LISN	SKP	SETG	EEQ	LINS	SVTK	CFSS	KN	SPL	1020
Db	961	SVNFSEAE	GVTE	YEA	ESQR	QPFV	KYAT	LISN	SKP	SETG	EEQ	LINS	SVTK	CFSS	KN	SPL	1020
QY	1021	KDSFSN	SSWE	IEA	QA	FFIL	SDOH	PNII	SPHL	TFSE	GLDEL	LKLE	GNFP	FEEN	DKK	SIYYL	1080
Db	1021	KDSFSN	SSWE	IEA	QA	FFIL	SDOH	PNII	SPHL	TFSE	GLDEL	LKLE	GNFP	FEEN	DKK	SIYYL	1080
QY	1081	GVTSIKK	RESG	VLLT	DKSR	VSC	PPAP	CLFT	DIRV	LQD	SCSH	FVEN	NINL	GTSS	KK	TFAS	1140
Db	1081	GVTSIKK	RESG	VLLT	DKSR	VSC	PPAP	CLFT	DIRV	LQD	SCSH	FVEN	NINL	GTSS	KK	TFAS	1140
QY	1141	YMPQF	QTC	STO	THK	IMEN	KM	CD	LT	V	1165						
Db	1141	YMPQF	QTC	STO	THK	IMEN	KM	CD	LT	V	1165						

RESULT

US-09-791-537-14096
; Sequence 14096, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14096
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-791-537-14096

Query Match 95.4%; Score 5967; DB 5; Length 1163;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1114; Conservative 18; Mismatches 31; Indels 2; Gaps 1;

QY	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWREKLSMPPNSTYDYELLPAGLSKNTSNS	60
Db	1	MICQKFCVLLHWEFICVITAFNLSYPITPWREKLSMPPNSTYDYELLPAGLSKNTSNL	60
QY	61	NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	NGHYETAVE--FNSSDTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSSVF	118
QY	121	QQIDANWNIOCLKGDLKLFICYVESLFKNLFERNYNYKVHLLVYLPEVLEDSPLVPQKGS	180
Db	119	QQMGANWNIOCLKGDLKLFICYVESLFKNPFKNYKHVKHLLVYLPEVLEDSPLVPQKGS	178
QY	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMVSQPINMVKPDPP	240
Db	179	FQMVHCNCSVHERCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMVSQPINMVKPDPP	238
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPFLQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	239	LGLRMEITDDGNLKISWSSPPLVPFPFLQYEVKYSENSTTVIREADKIVSATSLLVGDILP	298
QY	301	GSSYEVQVRGKRLDGPGIWSDSTPRVFTTQDVIFYPPPKILTSVGSNVSFHCIIYKKENKI	360
Db	299	GSSYEVQVRGKRLDGPGIWSDSTPHVFTTQDVIFYPPPKILTSVGSNVSFHCIIYKNENKI	358
QY	361	VPSKEIWWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH	420
Db	359	VSSKKIWWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH	418
QY	421	RYAELYVIDVNNISCETDGLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH	480
Db	419	RYAELYVIDVNNISCETDGHTKMTCRWSTNTIQSLAGSTLQLRYRSSLYCFDIPSIH	478

Matches 1114: Conservative 18; Mismatches 31; Indels 33; Gaps 2;			
Qy	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS	60
Db	1	MICQKFCVLLHWEFICVITAFNLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNL	60
Qy	61	NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	NGHYETAPE--FNSSDTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSSVF	118
Qy	121	QQIDANWNIQCWLKGDCLKLFICYVESLFKNLFRNRYNYKVHLLYVLPFVLEDSPLVPQKGS	180
Db	119	QQMGANWNIQCWLKGDCLKLFICYVESLFKNPKNYKKHKVHLLYVLPFVLEDSPLVPQKGS	178
Qy	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMSVQPINMVKPDP	240
Db	179	FQMVHCNCSVHERCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMSVQPINMVKPDP	238
Qy	241	LGLHMEITDDGNLKLISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	239	LGLRMEITDDGNLKLISWSSPPLVPFPLQYEVKYSENSTTVIREADKIVSATSLLVOGILP	298
Qy	301	GSSYEVOVRGKRLDGPGIWSDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI	360
Db	299	GSSYEVOVRGKRLDGPGIWSDWSTPHVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI	358
Qy	361	VPSKEIYVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECH	420
Db	359	VSSKKIYVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECH	418
Qy	421	RYAELYVIDVNNINISCETDGYLTAKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPS	480
Db	419	RYAELYVIDVNNINISCETDGHLTAKMTCRWSTNTIQSLAGSTLQLRYRRSSLYCFDIPS	478
Qy	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP	540
Db	479	PISKPKDCYLQSDGFYECVFQPIFLLSGYTMWIRINHPGLSLDSPPTCVLPDSVVKPLPP	538
Qy	541	SSVKAETINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMVEYDADAKSKSVSLPV	600
Db	539	SSVKAETIKNIGLLKISWEKPVFPENNLFQIRYGLSGKEIQWKMVDYDADAKSKSVSLPV	598
Qy	601	PDLCAVYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	599	PDFCAVYAVQVRCKRSDGLGLSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	658
Qy	661	TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI	720
Db	659	TLLWKPLMKNESLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI	718
Qy	721	GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED	780
Db	719	GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVILSWILSPSDYKLMYFIIWKNLNED	778
Qy	781	GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA	840
Db	779	GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFAQDNTEKHQND	838
Qy	841	GLYVIVPVIISSSILLGTLISHQRMKKLFWEDVPNPKNCWSWAQGLNFQK-----	891
Db	839	GLYVIVPVIISSSILLGTLILHQRMKKLFWEDVPNPKNCWSWAQGLNFQKIRGFVMLPR	898
Qy	892	-----PETFEHLFIKHTASVTCGPLLLEPETISEDISVDTSWK	929
Db	899	LVLNQAQVIHPPRPKVLQLQPETFEHLFIKHTASVTCGPLLLEPETISEDISVDTSWK	958
Qy	930	NKDEMMPTTVVSLSTTDLEKSGVCISDQFNSVNFSEAEGETVYTEDESQRQPFVKYATL	989
Db	959	NKDEMYPTTVVSLSTTDLEKSGVCISDQFNSVNFSEAEGETVYTEDESQRQPFVKYATL	1018
Qy	990	ISNSKPSGTGEEQGLINSSVTKCFSSKNSPLKDSFSNSSSWEIEAQAFFILSDQHPNIISP	1049
Db	1019	ISNSKPSGTDEEQGLINSSVTKCFSSKNSPLKDSFSNSSSWEIEAQAFFILSDQRPNIILP	1078

Qy	1050	HLTFSEGLDELLKLEGNFPENNDDKKSIIYYLGVTSIKKKRESGVLLTDKSRVSCFPAPCL	1109
Db	1079	HLTFSEGLDELLRLLEGNFPEENNDEKSIYYLGVTSIKKKRESGVLLTDKSRVLCFPAPCL	1138
Qy	1110	FTDIRVLQDSCSHFVENNINLGTSSKKTFASYMPQFQTCSTQTHKIMENKMCDLTV	1165
Db	1139	FTDIRVLQDSCSHFVENNFNLGTSSKKTFASYMPQFQTCSTQTHKIMENKMCDLTV	1194
RESULT 5			
US-09-791-537-95039			
; Sequence 95039, Application US/09791537			
; GENERAL INFORMATION:			
; APPLICANT: Bionomix, Inc.			
; APPLICANT: Debe, Derek			
; APPLICANT: Danzer, Joseph			
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME			
; TITLE OF INVENTION: METHODS OF USE THEREOF			
; FILE REFERENCE: 261/210			
; CURRENT APPLICATION NUMBER: US/09/791,537			
; CURRENT FILING DATE: 2001-02-22			
; NUMBER OF SEQ ID NOS: 153055			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 95039			
; LENGTH: 958			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-791-537-95039			

Query Match 77.3%; Score 4831.5; DB 5; Length 958;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 904; Conservative 5; Mismatches 24; Indels 25; Gaps 3;

Qy	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS	60
Db	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS	60
Qy	61	NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Qy	121	QQIDANWNIQCWLKGDCLKLFICYVESLFKNLFRNRYNYKVHLLYVLPFVLEDSPLVPQKGS	180
Db	121	QQIDANWNIQCWLKGDCLKLFICYVESLFKNLFRNRYNYKVHLLYVLPFVLEDSPLVPQKGS	180
Qy	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMSVQPINMVKPDP	240
Db	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMSVQPINMVKPDP	240
Qy	241	LGLHMEITDDGNLKLISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	241	LGLHMEITDDGNLKLISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Qy	301	GSSYEVOVRGKRLDGPGIWSDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI	360
Db	301	GSSYEVOVRGKRLDGPGIWSDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI	360
Qy	361	VPSKEIYVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECH	420
Db	361	VPSKEIYVWMNLAEKIPQSQYDVVSDHVSKVTFNLTNETKPRGKFTYDAVYCCNEHECH	420
Qy	421	RYAELYVIDVNNINISCETDGYLTAKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPS	480
Db	421	RYAELYVIDVNNINISCETDGYLTAKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPS	480
Qy	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP	540
Db	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP	540
Qy	541	SSVKAETINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMVEYDADAKSKSVSLPV	600

Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANENLTFSPMSKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMFLEWKNLNED 780
Db 721 GASVANENLTFSPMSKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMFLEWKNLNED 780
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK-----PE 893
Db 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKMLGSMFVK 900
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSWKNKDE 933
Db 901 SHHSLISSTQGHKHCGRPQGPLHRKTRDLCSLVYLLTLPPLLSYDPAKSPSVRNTQE 958

RESULT 6
US-09-791-537-95038
; Sequence 95038, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95038
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-95038

Query Match 77.2%; Score 4826; DB 5; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHJETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHJETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QQIDANWNIQCLWGLDKLFCYVESLFKNLFRNYKVVHLLYVLPVEVLESDPLVPQKGS 180
Db 121 QQIDANWNIQCLWGLDKLFCYVESLFKNLFRNYKVVHLLYVLPVEVLESDPLVPQKGS 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKLISWSSPPLVPFPLOQYQKYSNSTTVIREADKIIVSATSLLDVDSILP 300
Db 241 LGLHMEITDDGNLKLISWSSPPLVPFPLOQYQKYSNSTTVIREADKIIVSATSLLDVDSILP 300
QY 301 GSSYEVOVRGKRLDGPGLIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360

Db 301 GSSYEVOVRGKRLDGPGLIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
QY 361 VPSKEIYVWMNLAKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWMNLAKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVINISCEYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 421 RYAEIYVIDVINISCEYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANENLTFSPMSKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMFLEWKNLNED 780
Db 721 GASVANENLTFSPMSKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMFLEWKNLNED 780
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK 891
Db 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK 891

RESULT 7
US-09-791-537-114050
; Sequence 114050, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114050
; LENGTH: 958
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-114050

Query Match 77.1%; Score 4819.5; DB 5; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHJETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHJETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180

QY 181 FOMVHCNCVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FOMVHCNCVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPLMSVQPINMVKPDPP 240

QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVYSENSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVYSENSTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEYQVRGKRLDGGIWSDWSTPRVFTTQDVYFPPKILT SVGSNVSFHCYKKNKI 360
Db 301 GSSYEYQVRGKRLDGGIWSDWSTPRVFTTQDVYFPPKILT SVGSNVSFHCYKKNKI 360

QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIDVNIINISCE TDGYLT KMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
Db 421 RYAEIYVIDVNIINISCE TDGYLT KMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIWKKNLNE 780
Db 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIWKKNLNE 780

QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK-----PE 893
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKMLGSMFVK 900

QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSWKNKDE 933
Db 901 SHHSLISSTQGHKHCGRPQCP LHRKTRDCLSLVYLLTPPLLSYDPAKSPSVRNTOE 958

RESULT 8
US-09-791-537-114052
; Sequence 114052, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114052
; LENGTH: 906

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-114052

Query Match 77.0%; Score 4816; DB 5; Length 906;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60

QY 61 NGHYETAPEPKFNSSGTHFSNLKSTTFHCCFRSEQDRNCSLCA DNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAPEPKFNSSGTHFSNLKSTTFHCCFRSEQDRNCSLCA DNIEGKTFVSTVNSLVF 120

QY 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCWLKGDCLKLFICYVESLFKKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180

QY 181 FOMVHCNCVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
Db 181 FOMVHCNCVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPLMSVQPINMVKPDPP 240

QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVYSENSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVYSENSTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEYQVRGKRLDGGIWSDWSTPRVFTTQDVYFPPKILT SVGSNVSFHCYKKNKI 360
Db 301 GSSYEYQVRGKRLDGGIWSDWSTPRVFTTQDVYFPPKILT SVGSNVSFHCYKKNKI 360

QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIDVNIINISCE TDGYLT KMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
Db 421 RYAEIYVIDVNIINISCE TDGYLT KMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIWKKNLNE 780
Db 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIWKKNLNE 780

QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK--PETFEHL 898
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKMPGTKELL 900

RESULT 9
US-09-791-537-114053
; Sequence 114053, Application US/09791537

; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114053
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
us-09-791-537-114053

Query Match 77.0%; Score 4814; DB 5; Length 896;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTDYFLLPAGLSKNTSNS 60
QY 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTEFVSTVNSLVF 120
Db 61 NGHYTEAVEPKFNSSGTHFSNLSKATFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
QY 121 QQIDANNIQCWLKGDCLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANNIQCWLKGDCLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMSVQPINMVKPDPP 240
Db 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPLMSVQPINMVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEQVGRKLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEQVGRKLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
QY 361 VPSKEIYVWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAELYVIDVNIINISCEETDGYLTQVYSENSTTVIREADKIVSATSLLVDSILP 480
Db 421 RYAELYVIDVNIINISCEETDGYLTQVYSENSTTVIREADKIVSATSLLVDSILP 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMYEYDAKSVSPLV 600
Db 541 SSVKAEITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMYEYDAKSVSPLV 600
QY 601 PDLCAVYAVQVRCRRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMSKVNIVQSLAYSPLNSSCVIVSWILSPSDYKILMYFIIWKNLNED 780
Db 721 GASVANFNLTFSWPMSKVNIVQSLAYSPLNSSCVIVSWILSPSDYKILMYFIIWKNLNED 780

QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNKCSWAQGLNFQK 891
Db 841 GLYVIVPVISSILLGTLTLLISHQRMKKLFWEDVNPKNKCSWAQGLNFQK 891
RESULT 10
US-09-791-537-128089
; Sequence 128089, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 128089
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Rattus norvegicus
us-09-791-537-128089

Query Match 76.5%; Score 4786.5; DB 5; Length 1162;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 882; Conservative 119; Mismatches 160; Indels 5; Gaps 5;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTDYFLLPAGLSKNTSNS 60
QY 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 KGASEALVEAKFNSTGIYVSELSKTIFFHCCFGNEQGQNCALTGTGTEGTLASVVKPLVF 120
QY 121 QQIDANNIQCWLKGDCLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 RQLGVNWDIECWKMGDLTLFICHMEPLKPNFKNYDSKVHLLYDLPEVIDDLPLPPLKDS 180
QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMSVQPINMVKPDPP 240
Db 181 FQTVQCNCVSRE-CECHVPVPRAKVNYALLMYLEITSAGVSFQSPMSLQPMVLVVKPDPP 239
QY 241 LGLHMEITDDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
Db 240 LGLRMEVTDDGNLKIWSDSQTKAPFPLQYQVYLENS-TIVREAAEIVSDTSLVDSVLP 298
QY 301 GSSYEQVGRKLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
Db 299 GSSYEQVGRKLDGSGVWSWSLPLQFTTQDVMYFPPKILTSVGSNVSFHCYKKNENQT 358
QY 361 VPSKEIYVWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 ISSKQIYVWMNLAEKIPETQYNTVSDHISKVTFNLSKATRPGRGFTYDAVYCCNEQACHH 418
QY 421 RYAELYVIDVNIINISCEETDGYLTQVYSENSTTVIREADKIVSATSLLVDSILP 480
Db 419 RYAELYVIDVNIINISCEETDGYLTQVYSENSTTVIREADKIVSATSLLVDSILP 478
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMYEYDAKSVSPLV 600

Db 539 SSVKAEITINTGLLVSWKPVFPENNLFQIRYGLNGKEIQWKTHEVFDKSKSASLPV 598
QY 601 PDLCAVAVQVRCRLDGLGYWSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 SDCAVYVQVRCRLDGLGYWSNWSPPAYTLVMDVKNVPMRGPEFWRIMDGTKKERNV 658
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVEDVGNHKTFTFLWTEQAHTVTVLAINSI 720
Db 659 TLLWKPLMKNDSLCSVRRYVVKHRTAHNGTWSQDVGNQTNLTFLWAESAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 719 GASLVNFNLTFSWPMKVNIVQSLSAAYPLSSCVILSWTLSPNDYSLLYLVIEWKNLND 778
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMGVGPKKIINSFTQDDIEKHQSDA 840
Db 779 DGMKWLRIPSNVNKKYIHDNFIPIEKYQFSLYPIFMGVGPKKIINGFTKDDIAKQONDA 838
QY 841 GLYVIVPVIISILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPEFTEHLFI 900
Db 839 GLYVIVPIIISCVLLGLTLLISHQRMKKLFWDDVNPKNCSWAQGLNFQKPEFTEHLFT 898
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTT-DLEKGSVCISDQF 959
Db 899 KHAESVIFGPLLLEPEPVSEISVDTAWKNKDEMVPAAWVSLLTTPDSTRGICISDQC 958
QY 960 NSVNFSEAEGETEVTYDEDSQRPVVKYATLISNPKSETGEEQGLINSSVTKCFSSKNSP 1019
Db 959 NSANFSGAQSTQGTCEDECQSQPSVKYATLVSNVKTVEETDEEQGAIHSSVSQCIARKHSP 1018
QY 1020 LKDSFNSSSWEIEAQAFILSDQHPNIIISPHLTSEGLDELLKLEGNFPEENNKKSIYY 1079
Db 1019 LRQSFSSNSWEIEAQAFLLSDHPPNIVISPOLSFSG-GLDELLELEGNFPEENHGEKSVYY 1077
QY 1080 LGVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFA 1139
Db 1078 LGVSSGNKRENDMLLTDEAGVLCPPFAHCLFSDIRILQESCSHFVENNINLGTSG-KNFV 1136
QY 1140 SYMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1137 PYMPQFQSCSTHSHKIENKMCDLTV 1162

RESULT 11
US-09-791-537-57257
; Sequence 57257, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 2001-02-22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57257
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-57257

Query Match 76.4%; Score 4778.5; DB 5; Length 1162;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 881; Conservative 118; Mismatches 162; Indels 5; Gaps 5;
QY 1 MICQKFCVLLHWEFYVITAFNLSYPITPWRKLSKMPNPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MTCQKFVYVLLHWEFLYVITALNAYPTSPWRKLFCAAPPSTTDDSFSLPAGVPNNTSSL 60
QY 61.NGHYETAPEPKFNSSGTHFSNLSKTTTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120

Db 61 KGASEALVEAKFNSTGIYVSELSKTIHFCCFGNEQGNCSALTGNTGKTLASVVKPLVF 120
QY 121 QQIDANWNIQWLKGLKFLICYVESLEKFNFRNRYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 RQLGVNWDIECKWKGDLTLFICHMEPLKKNPKFNYSKVHLLYDLPEVIDDLPLPLKDS 180
QY 181 FQMVHCNCSVHECCCLVPPVPTAKLNDTLLMCLKITSGGVIFQSPMSVQPINVMVKPDPP 240
Db 181 FQTVQCNCVRE-CECHVPVPRAKVNYALLMYLEITSAGVSFQSPMSLQMLVVKPDPP 239
QY 241 LGLHMEITDDGNLKISWSSPPLVPPEPLQYQYKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 240 LGLRMEVTDGNNLKISWDSQTKAPFLQYVPVKYLENS-TIVREAAEIVSDTSLLVDSVLP 298
QY 301 GSSYEVQVRGKRLDGPISWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
Db 299 GSSYEVQVRSKRLDGSWSDWSLPQLFTTQDVMYFPPKILTSVGSNASECCYKKNENQT 358
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSKVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 ISSQIVWMNLAEKIPETQYNTVSDHISKVTFESNLKATPRGKFTYDAVYCCNEQACHH 418
QY 421 RYAELYVIDVNNINISCEITDGYLTMTKTCRWSTSTIQSLAESTLQLRHYRSSLYCSIDIPSIH 480
Db 419 RYAELYVIDVNNINISCEITDGYLTMTKTCRWSPSTIQSLVGVSTVQLRYHRRSLYCPDNPSIR 478
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 479 PTSELKNCVLQTDGFYECVFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 539 SSVKAEITINTGLLVSWKPVFPENNLFQIRYGLNGKEIQWKTHEVFDKSKSASLPV 598
QY 601 PDLCAVAVQVRCRLDGLGYWSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 SDCAVYVQVRCRLDGLGYWSNWSPPAYTLVMDVKNVPMRGPEFWRIMDGTKKERNV 658
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSVEDVGNHKTFTFLWTEQAHTVTVLAINSI 720
Db 659 TLLWKPLMKNDSLCSVRRYVVKHRTAHNGTWSQDVGNQTNLTFLWAESAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 719 GASLVNFNLTFSWPMKVNIVQSLSAAYPLSSCVILSWTLSPNDYSLLYLVIEWKNLND 778
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMGVGPKKIINSFTQDDIEKHQSDA 840
Db 779 DGMKWLRIPSNVNKKYIHDNFIPIEKYQFSLYPIFMGVGPKKIINGFTKDDIAKQONDA 838
QY 841 GLYVIVPVIISILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPEFTEHLFI 900
Db 839 GLYVIVPIIISCVLLGLTLLISHQRMKKLFWDDVNPKNCSWAQGLNFQKPEFTEHLFT 898
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTT-DLEKGSVCISDQF 959
Db 899 KHAESVIFGPLLLEPEPVSEISVDTAWKNKDEMVPAAWVSLLTTPDSTRGICISDQC 958
QY 960 NSVNFSEAEGETEVTYDEDSQRPVVKYATLISNPKSETGEEQGLINSSVTKCFSSKNSP 1019
Db 959 NSANFSGAQSTQGTCEDECQSQPSVKYATLVSNVKTVEETDEEQGAIHSSVSQCIARKHSP 1018
QY 1020 LKDSFNSSSWEIEAQAFILSDQHPNIIISPHLTSEGLDELLKLEGNFPEENNKKSIYY 1079
Db 1019 LRQSFSSNSWEIEAQAFLLSDHPPNIVISPOLSFSG-GLDELLELEGNFPEENHGEKSVYY 1077
QY 1080 LGVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFA 1139
Db 1078 LGVSSGNKRENDMLLTDEAGVLCPPFAHCLFSDIRILQESCSHFVENNINLGTSG-KNFV 1136
QY 1140 SYMPQFQTCSTQTHKIMENKMCDLTV 1165

Db 1137 PYMPQFQSCSTHSHKLIENKMCMLTV 1162

RESULT 12

US-09-791-537-65061

; Sequence 65061, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 65061

; LENGTH: 1162

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-791-537-65061

Query Match 76.2%; Score 4766.5; DB 5; Length 1162;
Best Local Similarity 75.4%; Pred. No. 0;
Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSMPNSTYDYFLLPAGLSKNTSNS 60

Db 1 MMCQKFYVLLHWEFLYVIAALNLAYPISPWKFLFCGPPNTDDSFSPAGAPNNASAL 60

QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTTFHCCFSEQRNCSLCAADNIEGKTFVSTVNSLVF 120

Db 61 KGASEAIVEAKFNSSGIYVPELSKTVFHCCEGNEQGNCSALTDNTEGKTLASVVVKASVF 120

QY 121 QQIDANWNIQWLKGLKLFICYVESLEFKNLERNYNYKVHLLYVLPVELEDSPLVPQKGS 180

Db 121 RQLGVNWDIECWMKGLTLFICHMEPLKPNPKNYDSKVHLLYDLPEVIDDSPLPLKDS 180

QY 181 FQMVHCNCSVHECECLVPVPTAKLNDTLMLCLKITSGVIFQSPMSVQPINMVKPDPP 240

Db 181 FQVQCNCSLRG-CECHVPVPRAKLNYALLMYLEITSAGVSFQSPMSLQPMVLVVKPDPP 239

QY 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVYSENSTVIREADKIVSATSLLVDSILP 300

Db 240 LGLHMEVTDGNLKISWDSQTMAPFPPLQYQVYLENS-TIVREAAEIVSATSLLVDSVLP 298

QY 301 GSSYEYQVRGKRLDGPISWSDWSTPRVFTTQDVYFPFKILTSGVNSVDFHCYKKNKI 360

Db 299 GSSYEYQVRGKRLDGSVWSDWSSPQVFTTQDVYFPFKILTSGVNSVDFHCYKKNKI 358

QY 361 VPSKEIVWMMNLAEKIPQSDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420

Db 359 ISSKQIVWWRNLAEKIPQSDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 418

QY 421 RYAELYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSLSLYCSDIPSIIH 480

Db 419 RYAELYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLVSTVQLYHRRSLYCPDPSIIH 478

QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVVKPLPP 540

Db 479 PTSEPKNCVLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVVKPLPP 538

QY 541 SSVKAEITINIGLLKISWEKVPFPENNLQFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600

Db 539 SNVKAETVNTGLLKVSWEKVPFPENNLQFQIRYGLSGKEIQWKTHEVFDKSKSASLLV 598

QY 601 PDLCAVYAVQVRCRRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

Db 599 SDLCAVYVQVRCRRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRKMDGDVTKKERNV 658

QY 661 TLLWKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTVLAINSI 720

Db 659 TLLWKPLTKNDLSLCSVRRYVVKHRTAHNGTWSDEVGNRTNLTFLWTEPAHTVTVLAVNSL 718

QY 721 GASVANFNLTFSWPMKSVNIYQSLASAYPLNSSCVIVSWILSPDYKLMFYFIEWKNLNED 780

Db 719 GASLVNFNLTFSWPMKSVSAVESLSAYPLSSSCVILSWILSPDDYSLLYLVVIEWKILNED 778

QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMGEGKPKIINSFTQDDIEKHQSDA 840

Db 779 DGMKWLRIPSNVKKFYIHDHFIPIEKYQFSLYPIFMGEGKPKIINGFTKDAIDKQONDA 838

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPEFHEHFI 900

Db 839 GLYVIVPVISSSILLGLTLLISHQRMKKLFWDDVNPKNCSWAQGLNFQKPEFHEHFI 898

QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTT-DLEKGSVCISDQF 959

Db 899 KHAESVIFGPLLLEPEPISEISVDTAWKNKDEMVPAAVMVSLLTTPDPPESSICISDQC 958

QY 960 NSVNFSEAEGETEVTYDESRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSP 1019

Db 959 NSANFSGSQSTQVTCEDQCQRPVVKYATLVSNDKLVETDEEQGLIHSPVSNICISSNHSP 1018

QY 1020 LKDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSGLDELKLEGNFPEENNDKKSIIY 1079

Db 1019 LRQSFSSSSWETEAQTFFLLSDQOPTMISPOLSFS-GLDELLEEGSFPEENHREKSVCY 1077

QY 1080 LGVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFA 1139

Db 1078 LGVTSVNRRESGVLLTGEAGILCTEPAQCLFSDIRILQERCSEHFVENNINLTSG-ENFY 1136

QY 1140 SYMPQFQTCSTQTHKIMENKMCMLTV 1165

Db 1137 PYMPQFQTCSTHSHKIMENKMCMLTV 1162

RESULT 13

US-09-791-537-26913

; Sequence 26913, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 26913

; LENGTH: 1174

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-791-537-26913

Query Match 76.2%; Score 4766.5; DB 5; Length 1174;
Best Local Similarity 75.4%; Pred. No. 0;
Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSMPNSTYDYFLLPAGLSKNTSNS 60

Db 1 MMCQKFYVLLHWEFLYVIAALNLAYPISPWKFLFCGPPNTDDSFSPAGAPNNASAL 60

QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTTFHCCFSEQRNCSLCAADNIEGKTFVSTVNSLVF 120

Db 61 KGASEAIVEAKFNSSGIYVPELSKTVFHCCEGNEQGNCSALTDNTEGKTLASVVVKASVF 120

QY 121 QQIDANWNIQWLKGLKLFICYVESLEFKNLERNYNYKVHLLYVLPVELEDSPLVPQKGS 180

Db 121 RQLGVNWDIECWMKGLTLFICHMEPLKPNPKNYDSKVHLLYDLPEVIDDSPLPLKDS 180

QY	181	FQMVHCNCSVHECCECLVPVPPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINVMVKPDPP	240
Db	181	: : : :	
QY	241	LGLHMEITDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	241	: : : : :	
QY	301	GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVIFPPKILTSVGSNVSEHCHYKKNKI	360
Db	301	: : : : :	
QY	361	VPSKEIYVWMNLAEKIPQSYQYDVVSDHVSQVTFNLTNETKPRGKFTYDAVYCNEHECHH	420
Db	361	: : : : :	
QY	421	RYAELYVIDVNISETDGYLTMTCTRWSTSTIQSLAESTLQRLYHRRSLYCSDIPIH	480
Db	421	: : : : :	
QY	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	540
Db	481	: : : : :	
QY	541	SSVKAELITINIGLLKISWEKPVFPENNLQFIQIRYGLSGKEVQWKMEYVDKSKSVSLPV	600
Db	541	: : : : :	
QY	601	PDLCAVAVQVRCRDLGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	601	: : : : :	
QY	661	TLWKPLMKNDSLCSQRYVYVINHHTSCNGTWSEDCVGNHTKFTFLWTEQAHTVTVLAINSI	720
Db	661	: : : : :	
QY	721	GASVANFNLTFSWPMKSNVIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE	780
Db	721	: : : : :	
QY	781	GEIKWLRISSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA	840
Db	781	: : : : :	
QY	841	GLYVIVPVIISILLGLTLLISHQRMKFLWEDVPNPKNCSWAQLNFQKPFTEHLFI	900
Db	841	: : : : :	
QY	901	KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTT-DLEKGSYCISDQF	959
Db	901	: : : : :	
QY	959	NSANFSGSQSTQVTCEDCQRQPSVKYATLVSNDRKLVTDEEQGFHSPVSNCLSSNHSP	1018
Db	959	: : : : :	
QY	1018	LKDSFNSSSWEIEAQAFFILSDOHPNIIISPHLTFSFGLDELLKLEGNFPEENNDKKSIIY	1079
Db	1018	: : : : :	
QY	1079	LRQSFSSSSWETEATFFLLSDQOPTMISPQLSFS-GLDELLELEGSFPEENHREKSVCY	1139
Db	1079	: : : : :	
QY	1139	LGVTSVNRRESGVLTLTGEAGILCTFPAQCLFSDIRILQERCSEHFVENNLGLTSG-ENFV	1196
Db	1139	: : : : :	
QY	1196	SYMPQFQTCSTQTHKINENKMCDLTV	1265
Db	1196	: : : : :	
QY	1265	PYMPQFQTCSTHSHKINENKMCDLTV	1332
Db	1265	: : : : :	

```

; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53431
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-53431

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Query Match	76.1%;	Score 4761.5;	DB 5;	Length 1162;
Best Local Similarity	75.3%;	Pred. NO. 0;		
Matches 878;	Conservative 116;	Mismatches 167;	Indels 5;	Gaps 5;

QY	1	MICQKFCWLLHWEFIYVITAFNLISYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS	60
Db	1	MMQCIFYWLLHWEFLYIAALNLAYPLSPWKFKLFCGPPNTTDDSFSPAGAPNNASAL	60
QY	61	NGHYETAPEPKFNSSGTHFNSLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	KGASEAIVEAKFNSSGIYVPELSKTFVHCCFGNEQGONCSALTDNTEGKTLASVVKASVF	120
QY	121	QQIDANWNIQCWLKGDCLKFICYVESLKFKNLFRNRYNYKVHLLYVLPPEVLEDSPLVPQKGS	180
Db	121	RQLGVNWDIECWMKGDITLFICHMEPLPKNPFKNYDSKVHLLYDLPEVIDDSDPLPLKDS	180
QY	181	FQMVHCNSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP	240
Db	181	FQTVQCNCSLRG-CECHVPVPRAKLYALLMYLEITSAGVSFQSPMLSLQPLMVVVKPDPP	239
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	240	LGLHMEVTDGNNLKISWDSQTMAPPLOQYQVKYLENS-TIVREAAEIVSATSLLVDSVLP	298
QY	301	GSSYEVOVRGKRDLGGPIWSDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKENKI	360
Db	299	GSSYEVOVRSKRDLGGVWSDWSSPOVFTTQDVYFPPKILTSVGSNASFHCYKKNENQI	358
QY	361	VPSKEIVWMNLAEKIPQSOQYDVVSDHVSKVTFNNLNETKPRGKFTYDAVYCNEHECHH	420
Db	359	ISSKQIVWWRNLAEKIPQISYIVSDRVSKVTFNSLKATRPRGKFTYDAVYCNEQAACH	418
QY	421	RYAELYVIDVNINISCETDGYLTMTCRWSTSTIQSLAESTLQLRYHRRSLYCSDIPSIH	480
Db	419	RYAELYVIDVNINISCETDGYLTMTCRWSPSTIQSLVGSTVQLRYHRRSLYCPDSPSIH	478
QY	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP	540
Db	479	PTSEPKNCVQLQSDGFYECVFPQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVVKPLPP	538
QY	541	SSVKAETINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMYEYDAKSXSLSLPV	600
Db	539	SNVKAETIVNTGLLKVSWEKVPFPENNLOFQIRYGLSGKEIOWKTHEVTFDAKSXSASLLV	598
QY	601	PDLCAVYAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	599	SNLCAVYVQVRCRRRLDGLGYWSNNSSPAYTLMVDMVKVPMRGPEFWRWKMDGDVTKKERNV	658
QY	661	TLLWKPLMKNDSLCSVQRYVINHHSTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVLAINSI	720
Db	659	TLLWKPLTKNDSLCSVRRYVVKHRTAHNGTWSDEVDGNRTNLTLFLWTEPAHTVTVLAVNSL	718
QY	721	GASVANFNLTFSWPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLINED	780
Db	719	GASLVNFNLTFSWPMSKVSAVESLSAYPLSSSCVILSWTSLPDDYSLLYLFIIEWKILINED	778

QY 781 GEIKWLRISSVKKYYIHDFIPIEKYQFSLYPIFMEGVGKPKIINSETQDDIEKHQSDA 840
Db 779 DGMKWLRISSVKKYYIHDFIPIEKYQFSLYPIFMEGVGKPKIINSETQDDIEKHQSDA 838
QY 841 GLYVIVPVISSILLGLTLLISHQRMKKLFWEDVPNPKNCSWAQLNFKQPETFEHLFI 900
Db 839 GLYVIVPVISSILLGLTLLISHQRMKKLFWDDVPNPKNCSWAQLNFKQPETFEHLFT 898
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPTTVVSLSTT-DLEKGSVCISDQF 959
Db 899 KHAESVIFGPLLEPEPISEIEISVDIAWKNKDEMVPAAVSLLLTTPDPRESSICISDQC 958
QY 960 NSVNFSEAEGETVYDEDESQRQPFVKYATLISNKPSETGEEQGLINSVTKCFSSKNSP 1019
Db 959 NSANFSGSQSTQVTCDEQCQRQPSVKYATLVSNDKLVTDEEQGFHSPVSNICISSNHSP 1018
QY 1020 LKDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIIY 1079
Db 1019 LRQSFSSSSWETEAEFTFLSDQOPTMISPLQSPS-GLDELLELEGSFPEENHREKSVCY 1077
QY 1080 LGVTSIKKRESGVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFA 1139
Db 1078 LGVTSVNRRESGVLLTGEAGILCTFPAQCLFSDIRILOERC SHFVENNINLGTSG-ENFV 1136
QY 1140 SYMPOFQTCSTQTHKIMENKMCDLTV 1165
Db 1137 PYMPOFQTCSTHSHKIMENKMCDLTV 1162
RESULT 15
US-09-791-537-45617
; Sequence 45617, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45617
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-45617

QY	301	GSSYEVQVRGKRLDGP	GIWSDWSTPRVFTTQDV	YFPFKILT	SVGSNVSFHC	YKKNKI	360
Db	299	GSSYEVQVRKRLDGS	WSDSSPQVFTTQDV	YFPFKILT	SVGSN	ASFHCYKKNQI	358
QY	361	VPSKEIVWMNLAEKIP	QSQYDVVSDHVKVTF	FNLNKPRGKFTY	DAVYC	NEHECHH	420
Db	359	ISSKQIVWMNLAEKIP	EIQYSIVSDRVSKVTF	SNLKATRPRGKFTY	DAVYC	CNEQACHH	418
QY	421	RYAELYVIDVNNISCE	TDGYLT	KMTCRWSTSTIQ	SIAESTLQ	LYHRSSLYCSDIPS	480
Db	419	RYAELYVIDVNNISCE	TDGYLT	KMTCRWSPSTIQ	SLVGSTVQ	LYHRSSLYCSDPS	478
QY	481	PISEPKDCYLQSDGF	ECIFQPIFLLSGYTM	WIRINHSLGSLDSP	PTCVLPDS	VVKPLPP	540
Db	479	PTSEPKNCVLRQDGF	ECVFOPIFLLSGYTM	WIRINHSLGSLDSP	PTCVLPDS	VVKPLPP	538
QY	541	SSVKAELITINIGLL	KISWEKPVFPENNLO	FQIRYGLSGKEVQW	KMYEYD	AKSKSVSLPV	600
Db	539	SNVKAELITVNTGLL	KYSWEKPVFPENNLO	FQIRYGLSGKEIQW	KTHEYF	DAKSKSASLLV	598
QY	601	PDLCAVYAVQVRCK	LDGLGYWSNPNPAYT	VVM	DIKVP	MGRGEFWRIINGDTM	660
Db	599	SDLCAVYVQVRCRR	LDGLGYWSNWSSPAYT	LVMDVKVPMRGPE	FWRKMDG	DVTKERNV	658
QY	661	TLWKPLMKNDSLCS	VQRYVINHHTSCNGT	WSEDVGNHTKFT	FLWTEQA	HTVTVLAINSI	720
Db	659	TLWKPLTKNDSLCS	VRYVVKHRTAHNGT	WSEDVGNRTNL	TFLWTEPA	HTVTVLAVNSL	718
QY	721	GASVANFNLTFSWP	MSKNIVQSLASAYPLN	SSCVIVSWILSP	SDYKLMYFI	IEWKLNED	780
Db	719	GASLVNFNLTFSP	WMSKVS	AVESLSAYPLSS	CVILSWTLP	SPDDYSLLYLVIEWK	778
QY	781	GEIKWLRISSVKKY	IHDHFIPIEKYQF	SLYPIFM	EGVGKPKIINS	FTQDOIEKHQSDA	840
Db	779	DGMKWLRIPSNVK	KFYIHDNFPIEKYQ	FSLYPVM	EGVGKPKIING	FTKDAIDKQONDA	838
QY	841	GLYVIVPVISSIL	LLGTLISHQRMK	KLFWEDVP	NPKNCSWAQ	GLNFQKPE	900
Db	839	GLYVIVPVISSCV	LLGTLISHQRMK	KLFWDDVP	NPKNCSWAQ	GLNFQKPE	898
QY	901	KHTASVTCGPLLE	PETISEDISVDT	SWKNKDEMP	TVVSLSTT-DLEK	GSVCISDQF	959
Db	899	KHAESVIFGPLLE	PEPISEISVDT	AWKNKDEM	VPAAMVSL	LLTTPDP	958
QY	960	NSVNFSEAE	TEVTYDE	SQRQPFVKYAT	LISN	SKPSETGEEQ	1019
Db	959	NSANFSGSQSTQ	VTCEDECQRQ	PSVKYAT	LVSN	DKLVE	1018
QY	1020	LKDSFSNSSWE	IEAQAF	ILLSDOHPNII	ISPHLTF	SEGLDELLK	1079
Db	1019	LRQSFSSSSW	ETEACQTF	LLSDQOPT	MISP	QLSFS-GLDE	1077
QY	1080	LGVT	SIKKRES	GVL	LTDKSRV	SCPPAPCLFTD	1139
Db	1078	LGVT	SVNRR	RES	GVL	LTGAGIL	1136
QY	1140	SYMPQ	FQTCSTQ	THKIMENK	MDLTV	1165	
Db	1137	PYMPQ	FQTCSTH	SHKIMENK	MDLTV	1162	

Search completed: August 15, 2002, 16:27:05
Job time: 370 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 16:22:20 ; Search time 91.6 Seconds
(without alignments)
2200.208 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEFIYVIT.....QTCSTQTHKIMENKMCDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ~~SPREMBL-19~~ *
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6254	100.0	1165	4 Q92921	Q92921 homo sapien
2	5967	95.4	1163	6 Q9MYL2	Q9MYL2 macaca mula
3	5941.5	95.0	1194	6 Q9MYL0	Q9MYL0 macaca mula
4	5269	84.3	1165	6 O02671	O02671 sus scrofa
5	4831.5	77.3	958	4 Q92920	Q92920 homo sapien
6	4826	77.2	896	4 Q92919	Q92919 homo sapien
7	4819.5	77.1	958	4 Q13592	Q13592 homo sapien
8	4816	77.0	906	4 Q13593	Q13593 homo sapien
9	4814	77.0	896	4 Q13594	Q13594 homo sapien
10	4761.5	76.1	1162	11 Q9QW3	Q9QW3 mus musculu
11	4591	73.4	925	6 Q9MYK9	Q9MYK9 macaca mula
12	4590	73.4	894	6 Q9MYL1	Q9MYL1 macaca mula
13	3970.5	63.5	848	6 Q9MZS2	Q9MZS2 sus scrofa
14	3729	59.6	895	11 Q62960	Q62960 rattus norv
15	2790.5	44.6	1147	13 Q9DDK1	Q9DDK1 meleagris g
16	2775	44.4	1148	13 Q9IBA7	Q9IBA7 gallus gall

17	2693	43.1	1146	13 Q918V6	Q918V6 gallus gall
18	1074	17.2	246	11 Q35773	Q35773 rattus norv
19	981.5	15.7	273	11 Q9QWV5	Q9QWV5 mus musculu
20	801	12.8	203	6 Q28604	Q28604 ovis aries
21	683	10.9	161	6 Q28606	Q28606 ovis aries
22	660.5	10.6	173	6 Q9XSN9	Q9XSN9 sus scrofa
23	616	9.8	147	6 Q95257	Q95257 sus scrofa
24	588	9.4	152	6 P79115	P79115 bos taurus
25	497	7.9	123	6 Q9N1F9	Q9N1F9 sus scrofa
26	477	7.6	121	6 O18980	O18980 bos taurus
27	456	7.3	145	13 Q9IA32	Q9IA32 gallus gall
28	444	7.1	881	13 Q57519	Q57519 xenopus lae
29	409.5	6.5	918	13 Q9W6U9	Q9W6U9 gallus gall
30	366	5.9	102	6 Q9XSH3	Q9XSH3 equus cabal
31	354	5.7	710	13 Q57520	Q57520 xenopus lae
32	325	5.2	74	11 Q9ERI4	Q9ERI4 rattus norv
33	312.5	5.0	1093	11 Q70535	Q70535 rattus norv
34	299	4.8	57	6 Q97778	Q97778 elephas max
35	299	4.8	57	6 Q97779	Q97779 loxodonta a
36	267	4.3	979	4 Q99650	Q99650 homo sapien
37	251.5	4.0	2302	11 Q88488	Q88488 rattus norv
38	232.5	3.7	970	11 Q88821	Q88821 mus musculu
39	228	3.6	971	11 Q70458	Q70458 mus musculu
40	213	3.4	57	13 Q90WY8	Q90WY8 gallus gall
41	197	3.1	861	6 Q9BEG2	Q9BEG2 bos taurus
42	195	3.1	1598	4 Q9P214	Q9P214 homo sapien
43	191.5	3.1	6875	6 Q28733	Q28733 oryctolagus
44	189.5	3.0	1114	5 Q9VSG6	Q9VSG6 drosophila
45	188	3.0	26926	4 Q10466	Q10466 homo sapien

ALIGNMENTS

RESULT 1
Q92921
ID Q92921 PRELIMINARY; PRT: 1165 AA.
AC Q92921;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96398968; PubMed=8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis.";
RL Curr. Biol. 6:1170-1180(1996)
DR EMBL; U66497; AAB07497.1; -;
DR HSSP; P16471; IBP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;

Query Match 100.0%; Score 6254; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSYPITPWFKLSMPPNSTYDFLLPAGLSKNTSNS 60
|||||

Db	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS	60
QY	61	NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
QY	121	QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS	180
Db	121	QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS	180
QY	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP	240
Db	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP	240
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	241	LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
QY	301	GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVYFPPPKILTSVGSNVSFHCYKKENKI	360
Db	301	GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVYFPPPKILTSVGSNVSFHCYKKENKI	360
QY	361	VPSKEIIVWMNLAEKIQSQDYDVSDHVSKVTFPNLNETKPRGKFTYDAVYCNEHECHH	420
Db	361	VPSKEIIVWMNLAEKIQSQDYDVSDHVSKVTFPNLNETKPRGKFTYDAVYCNEHECHH	420
QY	421	RYAELYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSII	480
Db	421	RYAELYVIDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSII	480
QY	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVVKPLPP	540
Db	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVVKPLPP	540
QY	541	SSVKAELITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVYDAKSVSPLV	600
Db	541	SSVKAELITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVYDAKSVSPLV	600
QY	601	PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	601	PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
QY	661	TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTVLAINSI	720
Db	661	TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTVLAINSI	720
QY	721	GASVANFLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMFYIETWKNLNE	780
Db	721	GASVANFLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMFYIETWKNLNE	780
QY	781	GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA	840
Db	781	GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA	840
QY	841	GLYVIVPVIISSSILLGTLIIHQRMKKLFWEDVPNPKNCSWAQLNFQKPFETFEHLFI	900
Db	841	GLYVIVPVIISSSILLGTLIIHQRMKKLFWEDVPNPKNCSWAQLNFQKPFETFEHLFI	900
QY	901	KHTASVTCGPPLLEPETISEDIVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN	960
Db	901	KHTASVTCGPPLLEPETISEDIVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN	960
QY	961	SVNFSEAGTEVTVEDESQRQPFVKYATLISNPKSETGEEQGLINSSVTKCFSSKNSPL	1020
Db	961	SVNFSEAGTEVTVEDESQRQPFVKYATLISNPKSETGEEQGLINSSVTKCFSSKNSPL	1020
QY	1021	KDSFSNSSWEIAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL	1080
Db	1021	KDSFSNSSWEIAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL	1080
QY	1081	GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS	1140
Db	1081	GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS	1140

QY	1141	YMPOFQTCSTQTHKIMENKMCDLTV	1165
Db	1141	YMPOFQTCSTQTHKIMENKMCDLTV	1165
RESULT	2		
Q9MYL2			
ID	Q9MYL2	PRELIMINARY;	PRT; 1163 AA.
AC	Q9MYL2;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	LEPTIN RECEPTOR LONG FORM.		
OS	Macaca mulatta (Rhesus macaque).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;		
OC	Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98408931; PubMed=9738551;		
RA	Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;		
RT	"Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA		
RT	expression in the adipose tissue of normal, hyperinsulinemic, and type		
RT	2 diabetic rhesus monkeys.";		
RL	Obes. Res. 6:353-360(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBBJ databases.		
DR	EMBL; AF222960; AAF34683.1; -.		
DR	HSSP; P16471; 1BP3.		
DR	InterPro; IPR002996; CR1A.		
DR	InterPro; IPR003961; FN_III.		
DR	InterPro; IPR003529; Hematopo_receptor_L_F2.		
DR	InterPro; IPR003531; Hematopo_receptor_S_F1.		
DR	Pfam; PF00041; fn3; 2.		
DR	SMART; SM00060; FN3; 1.		
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.		
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.		
KW	Receptor.		
SQ	SEQUENCE 1163 AA; 132295 MW; 6B7B89108F851895 CRC64;		

Query Match 95.4%; Score 5967; DB 6; Length 1163;
Best local Similarity 95.6%; Pred. No. 0;
Matches 1114; Conservative 18; Mismatches 31; Indels 2; Gaps 1;

QY	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS	60
Db	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNL	60
QY	61	NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	NGHYETAVE--FNSSDTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSSVF	118
QY	121	QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS	180
Db	119	QOMGANWNIQCWLKGLKLFICYVESLFKNFPKNYKHVHLLYVLPVLEDSPLVPQKGS	178
QY	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP	240
Db	179	FQMVHCNCSVHERCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP	238
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	239	LGLRMEITDDGNLKISWSSPPLVPFPLOYEVKYSENSTTVIREADKIVSATSLLVDCILP	298
QY	301	GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVYFPPPKILTSVGSNVSFHCYKKENKI	360
Db	299	GSSYEVQVRGKRLDGPGIWSDWSTPHVFTTQDVLYFPPPKILTSVGSNVSFHCYKKENKI	358

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QY 361 VPSKEIYVWMNLAEKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIYVWMNLAEKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAELYVIDVNNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 480
Db 419 RYAELYVIDVNNINISCETDGHLTKMTCRWSTNTIQSLAGSTLQLRYRRSSLYCFDIPSIIH 478
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 479 PISKPKDCYLQSDGFYECVFPQPIFLLSGYTMWIRINHPGLSGLDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYEVYDAKSXSLSLV 600
Db 539 SSVKAEIKNIGLLKISWEKPVFPENNLOFQIRYGLSGKEIQWKMYDYVYDAKSXSLSLV 598
QY 601 PDLCAVYAVQVRCKRLDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDFCAVYAVQVRCKRSDGLGLWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
QY 661 TLLWKPLMKNDLSLCSVQRYVINHHFTSCNGTWSQVGNHHTKFTFLWTEQAHTVTVLAINSI 720
Db 659 TLLWKPLMKNESLCSVQRYVINHHFTSCNGTWSQVGNHHTKFTFLWTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIVSWILSPDSYKLMYFIIWKNLNED 780
Db 719 GASVANFNLTFSWPMKSNIVQSLAYPLNSSCVILSWILSPDSYKLMYFIIWKNLNED 778
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 779 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFAQDNTTEKHQND 838
QY 841 GLYVIVPVLISSILLGLTLLISHQRMKKLFWEDEVNPNKNCNAOGLNFQKPEFHLFI 900
Db 839 GLYVIVPVLISSILLGLTLLILHQRMKKLFWEDEVNPNKNCNAOGLNFQKPEFHLFI 898
QY 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMMPPTVVSLSTTDLEKGSVCISDQFN 960
Db 899 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMVPPTVVSLSTTDLEKGSVCISDQFN 958
QY 961 SVNFSEAEGETVTEDESQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
Db 959 SVNFSEAEGETVTEDESQRQPFVKYATLISNSKPSSETDEEGLINSSVTKCFSSKNSPL 1018
QY 1021 KDSFNSNWEIEAQAFFILSDQHNPNIISPHLTFSEGLDELLKLEGNPPEENNDKKSIIYL 1080
Db 1019 KDSFNSNWEIEAQAFFILSDQRPNILPHLTFSEGLDELLRLEGNPPEENNDKKSIIYL 1078
QY 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1079 GVTSIKKRESGVLLTDKSRVLCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1138
QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1139 YMPQFQTCSTQTHKIMENKMCDLTV 1163

RESULT 3
Q9MYL0
ID Q9MYL0 PRELIMINARY; PRT: 1194 AA.
AC Q9MYL0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR LONG INSERT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
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RX MEDLINE=98408931; Pubmed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF225874; AAF35388.1;
DR HSSP; P16471; 1BP3.
DR InterPro; IPR02996; CR1A.
DR InterPro; IPR03961; FN_III.
DR InterPro; IPR03529; Hematopo_receptor_L_F2.
DR InterPro; IPR03531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;
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Query Match 95.0%; Score 5941.5; DB 6; Length 1194;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 1114; Conservative 18; Mismatches 31; Indels 33; Gaps 2;

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QY 1 MICQKFCVVLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60
Db 1 MICQKFCVVLHWEFICVITAFNLSYPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNL 60
QY 61 NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVE--FNSSDTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSVF 118
QY 121 QQIDANWNIOQWLKGDCLKFICYVESLFKNLFRNINYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 119 QQMGANWNIOQWLKGDCLKFICYVESLFKNPFKNYKHVHLLYVLPEVLEDSPLVPQKGS 178
QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMWKPDPP 240
Db 179 FQMVHCNCSVHERCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMWKPDPP 238
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIYSATSLLVDSILP 300
Db 239 LGLRMEITDDGNLKISWSSPPLVPFPPLQYQVKYSENSTTVIREADKIYSATSLLVDSILP 298
QY 301 GSSYEVOVRGKRDLGGPGIWSDWSTPRVFTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360
Db 299 GSSYEVOVRGKRDLGGPGIWSDWSTPHVFTQDVIYFPPKILTSVGSNVSFHCYKKNKI 358
QY 361 VPSKEIYVWMNLAEKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIYVWMNLAEKIPQSQDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAELYVIDVNNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 480
Db 419 RYAELYVIDVNNINISCETDGHLTKMTCRWSTNTIQSLAGSTLQLRYRRSSLYCFDIPSIIH 478
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
Db 479 PISKPKDCYLQSDGFYECVFPQPIFLLSGYTMWIRINHPGLSGLDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYEVYDAKSXSLSLV 600
Db 539 SSVKAEIKNIGLLKISWEKPVFPENNLOFQIRYGLSGKEIQWKMYDYVYDAKSXSLSLV 598
QY 601 PDLCAVYAVQVRCKRLDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDFCAVYAVQVRCKRSDGLGLWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
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QY 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 659 TLLWKPLMKNESLCSVQRYVINHHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 718
QY 721 GASVANENLTFSWPMSKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 719 GASVANENLTFSWPMSKVNIVQSLSAAYPLNSSCVILSWILSPSDYKLMYFIIEWKNLNE 778
QY 781 GEIKWLRISSSVKKYYIHDHFPIPIEKYQFSLYPIFMGVGPKKIINSETQDDIEKHQSDA 840
Db 779 GEIKWLRISSSVKKYYIHDHFPIPIEKYQFSLYPIFMGVGPKKIINSEFAQDNTEKHQND 838
QY 841 GLYVIVPVISSSILLGTLILSHQRMKKLFWEDVPNPKNCSSWAQGLNFQK----- 891
Db 839 GLYVIVPVISSSILLGTLILHQRMKKLFWEDVPNPKNCSSWAQGLNFQKIRGEVMLPR 898
QY 892 -----PETFEHLFIKHTASVTCGPPLLLEPETISEDISVDTSWK 929
Db 899 LVLNSQAQVIHPPRPKVLLEQPETFEHLFIKHTASVTCGPPLLLEPETISEDISVDTSWK 958
QY 930 NKDEMPPTTVSLLSTDLEKGSVCISDQFNSVNFSEAEGETVYDESEQRQPFVYATL 989
Db 959 NKDEMPPTTVSLLSTDLEKGSVCISDQFNSVNFSEAEGETVTECEDESQRQPFVYATL 1018
QY 990 ISNSKPSETGEOGLINSVTKCFSSKNSPLKDSFNSSSWEIEAQAFFILSDQHPNIISP 1049
Db 1019 ISNSKPSETDEEGLINSVTKCFSSKNSPLKDSFNSSSWEIEAQAFFILSDQHPNIILP 1078
QY 1050 HLTFSEGLDELLKLEGNFPEENNDKSIYYLGVTSIKKRESGVLLTDKSRVSCPPFPAPCL 1109
Db 1079 HLTFSEGLDELLRLEGNFPEENDEKSIYYLGVTSIKKRESGVLLTDKSRVLCPPFPAPCL 1138
QY 1110 FTDIRVLQDSCSHFVENNINLTSSKKTFAASYMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1139 FTDIRVLQDSCSHFVENNENLTSSKKTFAASYMPQFQTCSTQTHKIMENKMCDLTV 1194
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ID O02671 PRELIMINARY; PRT; 1165 AA.
AC O02671;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR.
GN LEPR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP
RC TISSUE=LIVER;
RA Men T.Y., Lacroix D.A., Ruiz-Cortes 2.F., Song J.H., Palin M.-F.,
RA Murphy B.D.;
RT "Porcine leptin (Ob) receptor complete coding sequence."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP
RX MEDLINE=97222487; PubMed=9069130;
RA Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.;
RT "The leptin receptor gene (LEPR) maps to porcine chromosome 6."
RL Mamm. Genome 8:226-226(1997).
DR EMBL; AF092422; AAC61766.1; -.
DR EMBL; U72070; AAC48707.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hmatopo_receptor_L_F2.
DR InterPro; IPR003531; Hmatopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 1165 AA; 132548 MW; 1BEB562FEA282F12 CRC64;
Query Match 84.3%; Score 5269; DB 6; Length 1165;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 980; Conservative 73; Mismatches 110; Indels 4; Gaps 4;
QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFLKSCMPNSTDYFLLPAGLSKNTSNS 60
Db 1 MTCPKFSVALLHWEFIYVITAFDLAYPITPWKFLKSCMPNTTYD-FLLPAGISKNTSTL 59
QY 61 NGHYTEAVEPKFNSSGTHFSNL-SKTTFHCCFRSQDRNCSLCADNIEGKTFVSTVNSLV 119
Db 60 NGHDEAVVETELNISCTYLSNLSKTTFHCCFWSEEDKNCVHADNIAKAFVSAVNSLV 119
QY 120 FQOIDANWNIQCWLKGLKLFICYVESLFKLNFRNYNYKVHLLYVLPEVLEDSPLVPQKG 179
Db 120 FQQTGANWNIQCWMKEDLKLFICYMESLFKPNFPNYDLKVHLLYVLLEVEGSPLLPQKG 179
QY 180 SFQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINMVKPDP 239
Db 180 SFQSVQCNCASARECCCHVPVSAAKLNYTLMLYKITSGGAVFHSPLMSVQPINVVKPDP 239
QY 240 PLGLHMEITDDGNLKISWSSPPLVPFPLOYQVQYKSENSTTVIREADKIVSATSLVDSIL 299
Db 240 PLGLHMEITDGNLKISWSSPTLVPFQLOYQVQYKSENSTTNMREADEIVSDTSLVDSVL 299
QY 300 PGSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPKPILT SVGSNVSEHCYKKNK 359
Db 300 PGSSYEVQVRGKRLDGPGIWSDWSTPFTTQDVIYFPKPILT SVGSNISRHCYKKNK 359
QY 360 IVPSKEIYVWMNLAEKIPQSQDYDVSDHVSKVTFPNLNETKPRGKFTYDAYVCCNEHECH 419
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QY 420 HRYAELYVIDVNIINISCTDGYLTMTKTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSI 479
Db 420 HRYAELYVIDVNIINISCTDGYLTMTKTCRWSTNATQSLVGSTLQLRYHRSSLYCSDVPSV 479
QY 480 HPISEPKDCYLQSDGFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLP 539
Db 480 HPISEPKDCQLQSDGFEYECIFQPIFLLSGYTMIRINHPGLSDSPPTCVLPDSVVKPLP 539
QY 540 PSSVKAETINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEVDYDAKSVSPL 599
Db 540 PSSVKAETAKIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKIYEVDYTKLKSTSLP 599
QY 500 VPDLCVAVAVQVRCKRLDGLGYWSNWSNPAYTVYMDIKVPMRGPEFWRIINGDTMKKEKN 659
Db 500 VPDLCVAVAVQVRCKRLDGLGYWSNWSNPAYTVYMDIKVPMRGPEFWRIINGDTMKKEKN 659
QY 660 VTLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAIN 719
Db 660 ITLLWKPLMKNDSLCSVRSYVVKHHTSRHGTSWSDVGNHTKLTFLWTEQAHSVTVLAVNS 719
QY 720 IGASVANENLTFSWPMSKVNIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 779
Db 720 IGASSANENLTFSWPMSKVNIVQSLSAAYPLNSSCVGLSWLLSPSDYNLMYLEWKILNE 779
QY 780 DGEIKWLRISSSVKKYYIHDHFPIPIEKYQFSLYPIFMGVGPKKIINSETQDDIEKHQSD 839
Db 780 DHEIKWLRIPSSVKKYYIHDHFPIPIEKYQFSLYPIFMGVGPKKIINSETQDG-EKHRND 838
QY 840 AGLYVIVPVISSSILLGTLILSHQRMKKLFWEDVPNPKNCSSWAQGLNFQKPFTEHLF 899
Db 839 AGLYVIVPVISSSILLGTLILSHQRMKKLFWEDVPNPKNCSSWAQGLNFQKPFTEHLF 898
QY 900 IKHTASVTCGPPLLLEPETISEDISVDTSWKNKDEMPPTTVVSLSTT-DLEKGSVCISDQ 958
Db 899 IKHTESVTFGPPLLLEPETISEDISVDTSWKNKDEMPPTTVVSLLLTTPDLEKSSICISDQ 958

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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:22:14 ; Search time 39.61 Seconds
(without alignments)
154.163 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKKPGESLKLT.....SSYTRSTRVFGGGLTLTVL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfilest1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	926.5	71.3	244	4	US-08-918-148-79	Sequence 79, Appl
2	892	68.6	249	4	US-08-918-148-74	Sequence 74, Appl
3	857	65.9	310	4	US-09-079-029-11	Sequence 11, Appl
4	824	63.4	258	2	US-08-665-202-5	Sequence 5, Appl
5	741.5	57.0	269	4	US-08-646-265A-109	Sequence 109, App
6	741.5	57.0	309	4	US-09-079-029-9	Sequence 9, Appl
7	734	56.5	312	4	US-09-079-029-10	Sequence 10, Appl
8	728.5	56.0	239	3	US-08-279-772A-8	Sequence 8, Appl
9	728.5	56.0	239	4	US-08-902-486-11	Sequence 11, Appl
10	728.5	56.0	599	1	US-08-463-163-3	Sequence 3, Appl
11	722	55.5	288	4	US-09-423-439-38	Sequence 38, Appl
12	722	55.5	673	4	US-09-423-439-32	Sequence 32, Appl
13	717	55.2	284	3	US-09-184-658-40	Sequence 40, Appl
14	714	54.9	280	4	US-09-260-527-1	Sequence 1, Appl
15	709	54.5	244	2	US-08-553-497A-20	Sequence 20, Appl
16	707	54.4	240	1	US-08-488-113B-148	Sequence 148, App
17	707	54.4	240	1	US-08-477-484B-148	Sequence 148, App
18	707	54.4	240	2	US-08-646-360-148	Sequence 148, App
19	707	54.4	240	4	US-08-839-765-148	Sequence 148, App
20	707	54.4	240	4	US-09-136-389-148	Sequence 148, App
21	706	54.3	267	4	US-09-485-737B-2	Sequence 2, Appl
22	706	54.3	541	4	US-09-485-737B-85	Sequence 85, Appl
23	706	54.3	711	4	US-09-485-737B-90	Sequence 90, Appl
24	699	53.8	245	4	US-08-918-148-78	Sequence 78, Appl
25	698	53.7	245	4	US-08-918-148-75	Sequence 75, Appl
26	697	53.6	246	2	US-08-553-497A-24	Sequence 24, Appl
27	693	53.3	245	4	US-08-918-148-76	Sequence 76, Appl

28	690	53.1	244	2	US-08-553-497A-22	Sequence 22, Appl
29	682	52.5	249	2	US-08-797-689-18	Sequence 18, Appl
30	680	52.3	281	4	US-09-025-769B-178	Sequence 178, App
31	679.5	52.3	281	4	US-09-423-439-44	Sequence 44, Appl
32	679.5	52.3	666	4	US-09-423-439-51	Sequence 51, Appl
33	676.5	52.0	270	2	US-08-652-507-2	Sequence 2, Appl
34	676	52.0	269	2	US-08-428-257A-72	Sequence 72, Appl
35	676	52.0	269	2	US-08-491-988-3	Sequence 3, Appl
36	676	52.0	402	2	US-08-491-988-9	Sequence 9, Appl
37	676	52.0	415	2	US-08-491-988-7	Sequence 7, Appl
38	676	52.0	435	2	US-08-491-988-5	Sequence 5, Appl
39	675.5	52.0	553	2	US-08-661-052-16	Sequence 16, Appl
40	675.5	52.0	553	4	US-09-188-082-16	Sequence 16, Appl
41	674	51.8	242	2	US-08-553-497A-26	Sequence 26, Appl
42	673	51.8	260	2	US-08-447-402-1	Sequence 1, Appl
43	669.5	51.5	244	4	US-08-918-148-77	Sequence 77, Appl
44	669.5	51.5	273	2	US-08-403-853-18	Sequence 18, Appl
45	665.5	51.2	240	4	US-09-485-737B-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-08-918-148-79
; Sequence 79, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 79
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
; US-08-918-148-79

Query Match 71.3%; Score 926.5; DB 4; Length 244;
Best Local Similarity 73.2%; Pred. No. 3.9e-64;
Matches 183; Conservative 18; Mismatches 38; Indels 11; Gaps 2;

QY	1	EVQLVQSGAEVKKPGESLKISCSGFTFSSYKMNWVROAPKGLKEMGIIPIFGTANY	60
DB	3	QVQLQSGPGGLVKPSETLSLTCTVSGDSISYWSWIRQPPKGLKWT-CYIYSGSTNY	61
QY	61	AQKFGKRVITADSTSTAYMELSSLRSEDTAVYYCARDRVVPATSLRGMDVWGQTT	120
DB	62	NPSLKSRTVISVPTSKSQFSLKLSVTADTAIVYYCARGY-----FDVWGRGTW	111
QY	121	VTVSSGGGGSGGGSGGSQSVLTQPASVSGSPGQITISCTGTSSDVGYVSWYQQ	180
DB	112	VTVSSGGGGSGGGSGGSQSVLTQPPVSGSPGQITISCTGTSSDVGYVSWYQQ	171
QY	181	HPGKAPKLMYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYCCSYTTRSTRV	240
DB	172	HPGKAPKLMYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYCCSYTTRSTRV	231
QY	241	FGGGLTLTVL 250	
DB	232	FGGGLTLTVL 241	

RESULT 2
US-08-918-148-74
; Sequence 74, Application US/08918148A


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; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-665-202-5

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Query Match	63.48;	Score 824;	DB 2;	Length 258;
Best Local Similarity	64.38;	Pred. No. 3e-56;		
Matches 164;	Conservative 38;	Mismatches 47;	Indels 6;	Gaps 3

[illegible]

RESULT 5
US-08-646-265A-109
; Sequence 109, Application US/08646265A
; Patent No. 6214973

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; APPLICANT: OHTOMO, Toshiniko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

COUNTRY: USA
ZIP: 20007-5109

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP94/017633
 ; FILING DATE: 19-OCT-1994

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 5-291078
 ; FILING DATE: 19-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEGNER, Harold C.
 ;

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1  REGISTRATION NUMBER: 25,258
2  REFERENCE/DOCKET NUMBER: 53466/184
3  TELECOMMUNICATION INFORMATION:
4  TELEPHONE: (202)672-5300
5  TELEFAX: (202)672-5399
6  TELEEX: 904136
7  INFORMATION FOR SEQ ID NO: 109:
8  SEQUENCE CHARACTERISTICS:
9  LENGTH: 269 amino acids
10 TYPE: amino acid
11 TOPOLOGY: linear
12 MOLECULE TYPE: protein
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14 US-08-646-265A-109

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Query Match	57.0%;	Score 741.5;	DB 4;	Length 269;
Best Local Similarity	61.6%;	Pred. No. 6.8e-50;		
Matches 154; Conservative	23;	Mismatches 60;	Indels 13;	Gaps 5;

[illegible]

RESULT 6
US-09-079-029-9
; Sequence 9, Application US/090790299
; Patent No. 6342369

; APPLICANT: Adams, Camilla W.
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Kim, Kyung J.
 ; TITLE OF INVENTION: Apo-2 Receptor
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

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; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/09/079,029
; FILING DATE:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416

Best Local Similarity 59.48; Pred. No. 1.7e-48;
Matches 149; Conservative 35; Mismatches 46; Indels 21; Gaps 6;

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Db	2	QVQLQDSGAELAKPGASVYKMSCKASGYTFTSYRMHWVKQRPQGGLIEMWICYINPSTGYTEY	61
QY	61	AQKFGQRTITADESTSTAYMELSLRSEDVAVYYCARDRVVVPATSLRCGM-DWGCGGT	119
		: :	
Db	62	NQKFKDKATLTADKSSSTAYMQLSLTFEEDSAVYYCARG-----GGVFEDWYCGGT	111
QY	120	TVTVSSGGGSGGGSGGGSGGSQSVLTQ--PASVSGSPGQSIITISCTGTSSDVGYGNYVSNY	178
		:	
Db	112	TLTVSSGGGSGGGSGGGSGGSQIVLTQSPALMASASPGEKVTITCSASSS----ISYMHNF	167
QY	179	QOHGKAPKLMITEGSKRPSGVSNRFSGSKSGSTASLTISGLQADEADYICSSYTTTRST	238
		:	
Db	168	QOKPQTSPKLMWITYTTSNLAGSVPARFSGSGSGSTSYSLTISRMEADEADATYYCHQ---RST	224
QY	239	--RVFGGGTKL 247	
Db	225	YPLTFGSGTKL 235	

RESULT 11

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US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
;
; GENERAL INFORMATION:
;
; APPLICANT: EMERY, Stephen Charles
;           BLAKEY, David Charles
;
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
;
; NUMBER OF SEQUENCES: 60
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: MS Word
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 38:
;
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 288 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

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Query match	55.58;	Score 722;	DB 4;	Length 288;
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QY	61 A Q F O G R V I T T A D E S T S T A Y M E L S L R S E D T A V Y C C A R D R V V P A T S L B G C M D W G O G T T	120
	: : : : : : : : : : : : : : : : : :	
D b	83 N E K F K K A T L T V D K S S T T A Y M O L S L T S E D S A V Y C C A R E R - - - A Y C Y D A M D Y W G O G T T	138
QY	121 V P V S S G G G G S G G G S G G G S Q S V L T Q - P A S V S G S P G O S I T I S C T G T S D V G - - - Y N Y V S	176
	: : : : : : : : : : : :	
D b	139 V P V S S G G G S G G G S G G G S D I E L S Q S P S L A V S A G E K V T M S C K S Q S L N S P T R K N Y L A	198
QY	177 W Y O Q H P G K A P K L M I Y E G S K R P S G V S N R F S G S K S G S T A S L T I S G L Q A E D E A D Y Y C - S S Y T T	235
	: : : : : : : : : : : : : : : :	
D b	199 W Y O Q R P G Q S P K L L I Y W A S T R T S G V P D R F T G S G S G T D F T L T I S S Y Q A E D L A I Y C K O S Y T L	258
QY	236 R S T R V F G G G T K L T V	249
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D b	259 R T - - - F G G G T K L E I	269

RESULT 12
US-09-423-439-32

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1  Sequence 32, Application US/09423439
2  Patent No. 6339070
3
4  GENERAL INFORMATION:
5  APPLICANT: EMERY, Stephen Charles
6             BLAKEY, David Charles
7  TITLE OF INVENTION: CHEMICAL COMPOUNDS
8  NUMBER OF SEQUENCES: 60
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Pillsbury Winthrop, L.L.
11 STREET: 1100 New York Ave., N.W.
12 CITY: Washington
13 STATE: D.C.
14 COUNTRY: U.S.A.
15 ZIP: 20005
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: MS Word
22
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/09/423,439
25 FILING DATE: 09-No. 6339070-1999
26 CLASSIFICATION: <unknown>
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: PCT/GB98/01294
30 FILING DATE: 05-MAY-1998
31 APPLICATION NUMBER: GB 9709421.3
32 FILING DATE: 10-MAY-1997
33
34 INFORMATION FOR SEQ ID NO: 32:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 673 amino acids
37 TYPE: amino acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: protein
41 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
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Query Match 55.58; Score 722; DB 4; Length 673;

[illegible]

APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 54.5%; Score 709; DB 2; Length 244;
Best Local Similarity 56.8%; Pred. No. 1.9e-47;
Matches 147; Conservative 37; Mismatches 49; Indels 26; Gaps 7;

QY 1 EVOLVQSGAEVKKPQESLKISCQSGFTFSYKMNWVROAPGKLEWNGCIIPFGTANY 60
DB 1 EVOLQQSGAELVKPGASVKLSCKASGYTFTSHMHWVKORAGQGLEWIGFENPNSGRITNY 60
QY 61 AOKFQGRVTTADESTSTAYMELSLRSEDTAVYYCA-RD-----RVVVPATSLRGMDV 114
DB 61 NEKFKSKATLIVDKSSSTAYMQLSLTSEDSAVYYCASRDYDYDGRY-----FDY 110
QY 115 WGQGTIVTVSSGGGSGGGGSGGGSQSVLTQ-PASVSGSPGQSTITSGTGTSSDVGGYN 173
DB 111 WGQGTIVTVSSGGGSGGGGSGGSDIELTQSPAIMASASPGKVTMTCSASSS---VS 166
QY 174 YVSWYQOHPRKAPKLMIEGSKRPSGVSNRPSGSKSGSTASLTISGLQADEADYYC--- 230
DB 167 YMYWYQKPGSSPRLLIYDTSNLAGVPPVPRSGSGSGTSLTISRMEADAATYYCQGM 226
QY 231 SSYTRSTRVFGGGLTV 249

Db 227 SSYPMPWT--FGGGLTKLEI 243

Search completed: August 15, 2002, 16:22:15
Job time: 425 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:27:06 ; Search time 111.01 Seconds
(without alignments)
520.399 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SSYTRSTRVFGGTKLTVL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 698052 seqs, 231078099 residues

Total number of hits satisfying chosen parameters: 698052

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1163	89.5	249	5	US-09-959-373A-2	Sequence 2, Appl
2	1092.5	84.0	242	1	PCT-US02-16106-16	Sequence 16, Appl
3	1092.5	84.0	242	6	US-10-151-882-16	Sequence 16, Appl
4	1012	77.8	272	5	US-09-791-537-845	Sequence 845, App
5	980	75.4	245	6	US-10-039-785-47	Sequence 47, Appl
6	980	75.4	245	6	US-10-139-785-47	Sequence 47, Appl
7	967	74.4	245	1	PCT-US02-16106-15	Sequence 15, Appl
8	967	74.4	245	6	US-10-151-882-15	Sequence 15, Appl
9	966	74.3	254	5	US-09-791-537-32035	Sequence 32035, A
10	965	74.2	245	6	US-10-039-785-51	Sequence 51, Appl
11	965	74.2	245	6	US-10-139-785-51	Sequence 51, Appl
12	948	72.9	245	6	US-10-039-785-43	Sequence 43, Appl
13	948	72.9	245	6	US-10-139-785-43	Sequence 43, Appl
14	943.5	72.6	248	1	PCT-US02-16106-19	Sequence 19, Appl
15	943.5	72.6	248	6	US-10-151-882-19	Sequence 19, Appl
16	939	72.2	245	6	US-10-039-785-42	Sequence 42, Appl
17	939	72.2	245	6	US-10-139-785-46	Sequence 46, Appl
18	939	72.2	245	6	US-10-139-785-42	Sequence 42, Appl
19	939	72.2	245	6	US-10-139-785-46	Sequence 46, Appl
20	937	72.1	245	6	US-10-039-785-52	Sequence 52, Appl
21	937	72.1	245	6	US-10-139-785-52	Sequence 52, Appl
22	934.5	71.9	248	1	PCT-US02-16106-17	Sequence 17, Appl
23	934.5	71.9	248	6	US-10-151-882-17	Sequence 17, Appl
24	928	71.4	245	6	US-10-039-785-45	Sequence 45, Appl
25	928	71.4	245	6	US-10-039-785-48	Sequence 48, Appl
26	928	71.4	245	6	US-10-139-785-45	Sequence 45, Appl

27	928	71.4	245	6	US-10-139-785-48	Sequence 48, Appl
28	923	71.0	245	6	US-10-039-785-49	Sequence 49, Appl
29	923	71.0	245	6	US-10-139-785-49	Sequence 49, Appl
30	903	69.5	246	5	US-09-791-537-70804	Sequence 70804, A
31	896.5	69.0	252	1	PCT-US02-11474-73	Sequence 73, Appl
32	896.5	69.0	252	6	US-10-120-414-73	Sequence 73, Appl
33	894	68.8	249	1	PCT-US02-16106-18	Sequence 18, Appl
34	894	68.8	249	6	US-10-151-882-18	Sequence 18, Appl
35	856	65.8	241	1	PCT-US02-16106-21	Sequence 21, Appl
36	856	65.8	241	6	US-10-151-882-21	Sequence 21, Appl
37	848.5	65.3	252	1	PCT-US02-16106-14	Sequence 14, Appl
38	848.5	65.3	252	6	US-10-151-882-14	Sequence 14, Appl
39	836.5	64.3	254	1	PCT-US02-16106-24	Sequence 24, Appl
40	836.5	64.3	254	6	US-10-151-882-24	Sequence 24, Appl
41	836	64.3	253	1	PCT-US02-11474-76	Sequence 76, Appl
42	836	64.3	253	6	US-10-120-414-76	Sequence 76, Appl
43	833.5	64.1	252	1	PCT-US02-16106-13	Sequence 13, Appl
44	833.5	64.1	252	6	US-10-151-882-13	Sequence 13, Appl
45	826.5	63.6	240	1	PCT-US02-16106-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-959-373A-2
; Sequence 2, Application US/09959373A
; GENERAL INFORMATION:
; APPLICANT: Zardi, Luciano
; TITLE OF INVENTION: A tenascin-c isoform as a marker for neoplasias
; FILE REFERENCE: 1875PT
; CURRENT APPLICATION NUMBER: US/09/959,373A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: FI99A000094
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-959-373A-2

Query Match	89.5%;	Score 1163;	DB 5;	Length 249;
Best Local Similarity	89.6%;	Pred. No. 2.3e-62;		
Matches	225;	Conservative 11;	Mismatches 11;	Indels 4; Gaps 2;
QY	1	EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNVRQAPGKGLEWMGGIPIFGTANY 60		
Db	1	QVQLVQSGAEVKKPGSSVKVSKASGDTFSSYKMNVRQAPGKGLEWMGGIPIFGTANY 60		
QY	61	AQKFOGRVTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGG-MDVWGQGT 119		
Db	61	AQKFOGRVTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGG-MDVWGQGT 117		
QY	120	TVTSSGGGGGGGGGSGGSGSVLTQPASVSGSPGQITISCTGTSSDVGGYNYVSWYQ 179		
Db	118	MVTSSGGGGGGGGGSGGSGSVLTQPASVSGSPGQITISCTGTSSDVGGYNYVSWYQ 177		
QY	180	QHPGKAPKLMIEGSKRPSGVSNRFGSGSKSGSTASLTISGLQAEDEADYYCSYTRSTR 239		
Db	178	QHPGKAPKLMIEGSKRPSGVSNRFGSGSKSGNTASLTISGLQAEDEADYYCSYTRSTR 237		
QY	240	VFGGGTKLTVL 250		
Db	238	VFGGGTKLTVL 248		

RESULT 2
PCT-US02-16106-16
; Sequence 16, Application PC/TUS0216106
; GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554PCT
CURRENT APPLICATION NUMBER: PCT/US02/16106
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 242
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A027A11 scFv
PCT-US02-16106-16

Query Match 84.0%; Score 1092.5; DB 1; Length 242;
Best Local Similarity 83.6%; Pred. No. 3.5e-58;
Matches 209; Conservative 15; Mismatches 17; Indels 9; Gaps 1;
QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
Db 1 QVQLQSGAEVKKPGSSVKVSKASGGTFSTYAITWVRQAPGQGLEWMGDIIPVFGIPNY 60
QY 61 AQKFGQRVITADESTSTAYMELSSLRSEDVAVYYCARDRVVVPATSLRGGMDVWGQGT 120
Db 61 AQMFQDRVTITADESTSTAYLELNSLGAEDTAVYYCARG-----SQAFEIWGKGT 111
QY 121 VTVSSGGGGGGGGGGSQSVLTQPASVSGSPGQSIITISCTGTSSDVGGYNYVSWYQQ 180
Db 112 VTVSSGGGGGGGGGGSQSVLTQPASVSGSPGQSIITISCTGTSSDVGGYNYVSWYQQ 171
QY 181 HPGKAPKLMIEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTTRSTRV 240
Db 172 HPGKAPKLMIEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTTRSTRV 231
QY 241 FGGGTKLTVL 250
Db 232 FGGGTKLTVL 241

RESULT 3
US-10-151-882-16
Sequence 16, Application US/10151882
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 242
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A027A11 scFv
US-10-151-882-16

Query Match 84.0%; Score 1092.5; DB 6; Length 242;
Best Local Similarity 83.6%; Pred. No. 3.5e-58;
Matches 209; Conservative 15; Mismatches 17; Indels 9; Gaps 1;
QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
Db 1 QVQLQSGAEVKKPGSSVKVSKASGGTFSTYAITWVRQAPGQGLEWMGDIIPVFGIPNY 60

QY 61 AQKFGQRVITADESTSTAYMELSSLRSEDVAVYYCARDRVVVPATSLRGGMDVWGQGT 120
Db 61 AQMFQDRVTITADESTSTAYLELNSLGAEDTAVYYCARG-----SQAFEIWGKGT 111
QY 121 VTVSSGGGGGGGGGGSQSVLTQPASVSGSPGQSIITISCTGTSSDVGGYNYVSWYQQ 180
Db 112 VTVSSGGGGGGGGGGSQSVLTQPASVSGSPGQSIITISCTGTSSDVGGYNYVSWYQQ 171
QY 181 HPGKAPKLMIEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTTRSTRV 240
Db 172 HPGKAPKLMIEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTTRSTRV 231
QY 241 FGGGTKLTVL 250
Db 232 FGGGTKLTVL 241

RESULT 4
US-09-791-537-845
Sequence 845, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 845
LENGTH: 272
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-845

Query Match 77.8%; Score 1012; DB 5; Length 272;
Best Local Similarity 77.6%; Pred. No. 2.5e-53;
Matches 194; Conservative 19; Mismatches 33; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
Db 3 EVQLVESGGGLVKPGGSLRLSCAASGFTFSNYSMNWVRQAPGKGLEWSSSSSYIYY 62
QY 61 AQKFGQRVITADESTSTAYMELSSLRSEDVAVYYCARDRVVVPATSLRGGMDVWGQGT 120
Db 63 ADFVKGRTISRDNKNSLYLQMNLSLRAEDTAVYYCARSSI---TIFGGMDVWGRGTL 118
QY 121 VTVSSGGGGGGGGGGSQSVLTQPASVSGSPGQSIITISCTGTSSDVGGYNYVSWYQQ 180
Db 119 VTVSSGGGGGGGGGGSQSVLTQPASVSGSPGQSIITISCTGTSSDVGGYNYVSWYQQ 178
QY 181 HPGKAPKLMIEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTTRSTRV 240
Db 179 HPGKAPKLMIEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTTRSTRV 238
QY 241 FGGGTKLTVL 250
Db 239 FGGGTKLAVL 248

RESULT 5
US-10-039-785-47
Sequence 47, Application US/10039785
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07

Db 1 QVOLVQSGAEVKKPGSSVKVSCKASGGTFSSYGIRWVRQAPGQGLEWMGGIPIFGTANY 60

QY 61 AQKFQGRVTITADESTSTAYMELSSRLSRSEDPAVYYCARDRVVVPATSLRGMDVWGQGT 120

Db 61 AQKFQGRVTITADEYTSTAYMELSSRLSRSEDPAVYYCARSNPQYDA-----FDIWGQGT 114

QY 121 VTVSSGGGGGGGGGGSSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYVSWYQQ 180

Db 115 VTVSSGGGGGGGGGGSSYVLTQPPSVSGTPGQRVTVSCSGGRSNIGS-NTVKWYQQ 173

QY 181 HPGKAPKLMIEGSKRPSGVSNRFGSKSGSTASLTISGLQAEDEADYYCSSYTRSTR- 239

Db 174 LPGTAPKLLIYGNDQRPSPGVPDRFSGSKSGNTASLTVSGLQVEDEADYYCQSYDS-SLRG 232

QY 240 -VEGGGTKLTVL 250

Db 233 SVFGGGTKLTVL 244

RESULT 8

US-10-151-882-15

; Sequence 15, Application US/10151882

; GENERAL INFORMATION:

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

; FILE REFERENCE: PF554

; CURRENT APPLICATION NUMBER: US/10/151,882

; CURRENT FILING DATE: 2002-05-22

; PRIOR APPLICATION NUMBER: 60/293,100

; PRIOR FILING DATE: 2001-05-24

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 245

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: A004G02 scFv

US-10-151-882-15

Query Match 74.4%; Score 967; DB 6; Length 245;

Best Local Similarity 75.8%; Pred. No. 1.1e-50;

Matches 191; Conservative 19; Mismatches 32; Indels 10; Gaps 4;

QY 1 EVQLVQSGAEVKKPGESLKISCQSGGTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60

Db 1 QVOLVQSGAEVKKPGSSVKVSCKASGGTFSSYGIRWVRQAPGQGLEWMGGIPIFGTANY 60

QY 61 AQKFQGRVTITADESTSTAYMELSSRLSRSEDPAVYYCARDRVVVPATSLRGMDVWGQGT 120

Db 61 AQKFQGRVTITADEYTSTAYMELSSRLSRSEDPAVYYCARSNPQYDA-----FDIWGQGT 114

QY 121 VTVSSGGGGGGGGGGSSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYVSWYQQ 180

Db 115 VTVSSGGGGGGGGGGSSYVLTQPPSVSGTPGQRVTVSCSGGRSNIGS-NTVKWYQQ 173

QY 181 HPGKAPKLMIEGSKRPSGVSNRFGSKSGSTASLTISGLQAEDEADYYCSSYTRSTR- 239

Db 174 LPGTAPKLLIYGNDQRPSPGVPDRFSGSKSGNTASLTVSGLQVEDEADYYCQSYDS-SLRG 232

QY 240 -VEGGGTKLTVL 250

Db 233 SVFGGGTKLTVL 244

RESULT 9

US-09-791-537-32035

; Sequence 32035, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/2110

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 32035

; LENGTH: 254

; TYPE: PRT

; ORGANISM: synthetic construct

US-09-791-537-32035

Query Match 74.3%; Score 966; DB 5; Length 254;

Best Local Similarity 73.1%; Pred. No. 1.3e-50;

Matches 190; Conservative 19; Mismatches 33; Indels 18; Gaps 2;

OY 1 EVQLVQSGAEVKKPGESLKISCQSGGTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60

Db 2 QVOLVESGGGVVQPGRSLRLSCAASGFFTRNYGVHVRQAPGKGLEWAVISYDGSNKYY 61

OY 61 AQKFQGRVTITADESTSTAYMELSSRLSRSEDPAVYYCARDRVVVPATSLRG----- 111

Db 62 ADSVKGRFTISRDNKNTLYLQMNSLRVEDPAVYYCAR-----RWYGGSGYWGHFYS 113

OY 112 -MDVWGQGTTVTVSSGGGGGGGGGGSSQSVLTQPASVSGSPGQSITISCTGTSSDV 170

Db 114 YMDGWGKGTKVTVSSGGGGGGGGGGSSQSVLTQPASVSGSPGQSITISCTGTSSDV 173

OY 171 GYNVSWYQQHPGKAPKLMIEGSKRPSGVSNRFGSKSGSTASLTISGLQAEDEADYYC 230

Db 174 GYNVSWYQQHPGKAPKLMIEGSKRPSGVSNRFGSKSGSTASLTISGLQAEDEADYYC 233

OY 231 SSYTRSTRVFGGTKLTVL 250

Db 234 SSYTRSTRVFGGTRLTVL 253

RESULT 10

US-10-039-785-51

; Sequence 51, Application US/10039785

; GENERAL INFORMATION:

; APPLICANT: Salcedo et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: PF550

; CURRENT APPLICATION NUMBER: US/10/039,785

; CURRENT FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: 60/369,860

; PRIOR FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 60/341,237

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 60/331,310

; PRIOR FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/331,044

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 60/327,364

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/323,807

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/309,176

; PRIOR FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 60/294,981

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/293,473

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 51

; LENGTH: 245

; TYPE: PRT

; ORGANISM: Artificial sequence

Db	113	LVTVSSGGGGGGGGGSAQALTPASVSGSPQOSITISCTGTSDDIGAYKYVSWY	172
QY	179	QQHPGKAPKLMIEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEADYVCSSYTRST	238
Db	173	QQHPGKAPKLVIEVSNRPSGVSSRFSKSGQTASLTISGLQADDEADYVCNSYQGYNT	232
QY	239	RVFGGGTKLTVL	250
Db	233	WVFGGGTKVTVL	244

RESULT 13.
US-10-139-785-43
; Sequence 43, Application US/10139785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785

Query Match 72.9%; Score 948; DB 6; Length 245;
Best Local Similarity 74.6%; Pred. NO. 1.5e-49;
Matches 188; Conservative 20; Mismatches 34; Indels 10; Gaps 3;

QY	1	EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNVVRQAAPGKGLEWMGGIIPFGTANY	60
Dd	1	EVQLVQSGAEVKMPGASVKLSRVSGDTFTAYFIHWVRQAAPGGLEWGMGFNPISGTAGS	60
QY	61	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVVPATSLRGG-MDVWGQG	119
Dd	61	AEKFRGRVAMTRDTSISTAYMELNRLTFDDTAVYYCARQH-----RGNTFDPPWGQG	112
QY	120	TVTVSSGGGGGGGGGGGS-QSVLTQPASVSGSPGQSITISCTGTSSTDVGGINYVS	178
Dd	113	LVTVSSGGGGGGGGGGGAQSAQTQPASVSGSPGQSITISCTGTSSTDIGAKYIVSWY	172
QY	179	QQHPGKAPKLMIYEGSKRRPSGVSNRFSGSKSGSTASLTISGLQAEADAYC	238
Dd	173	QQHPGKAPKLVIYEVSNNRPSPGVSSRFSGSKSGQTASLTISGLQAEADAYCNSYQGYNT	232
QY	249	RVFGGGTKLTVL	250

Best Local Similarity 73.9%; pred. No. 2.8e-49;				
Matches 187; Conservative 26; Mismatches 31; Indels 9; Gaps 4;				
QY	1	EVQLVQSGAEVKKPESLKIS	CGSGFTFSYKMNWVRQAPGK	GLEWMMGGIPIFGTANY 60
Db	1	EVQLVQSGAEVKKPESSVK	VSCKASGGTFSNYAISWVRQAP	QGQGLEWMMGGIPIFLDTPNY 60
QY	61	AQKFGQGRVTITADESTST	AYMELSSLRSEDTAVYYCARD	RVVVPATSLRGMDVWGQGT 120
Db	61	AQKFGQGRVTITADESTST	AYMELSSLRSEDTAVYYCARGN	-----TGPR-PFDPWGKGT 114
QY	121	VTVSSGGGGGGGGGGGS-Q	SVLTQPASVSGSPGQSITIS	CTGTSSDVGGYNVVSWYQ 179
Db	115	VTVSSGGGGGGGGGGGSA	QAVLTQPSVSGAPGQRTVSC	TGSSSNIGAGYEVNWIYQ 174
QY	180	QHPGKAPKLMIEGSKRPS	GVSNRFSGSKSGSTASLTIS	GLQAEDEADYYCSSYTT--RS 237
Db	175	QLPGTAPKLLIYGDTNR	PSGVDPDRFSGSKSGTSAS	LAITGLQAEDEANYCQSYDSGPGG 234
QY	238	TRVFGGGTKLTVL	250	
Db	235	PVVFEGGTKLTVL	247	

Search completed: August 15, 2002, 16:27:07
Job time: 372 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:34:04 ; Search time 410.32 Seconds
(without alignments)
214.455 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKKPGESLK.....SSYTRSTRVFGGTKLTVL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
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19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1300	100.0	250	11 US-08-779-457-49	Sequence 49, Appl
2	1152.5	88.7	254	1 PCT-US01-19110-1412	Sequence 1412, Ap
3	1152.5	88.7	254	22 US-09-880-748-1412	Sequence 1412, Ap
4	1149	88.4	253	1 PCT-US01-19110-1813	Sequence 1813, Ap
5	1149	88.4	253	22 US-09-880-748-1813	Sequence 1813, Ap
6	1147.5	88.3	252	1 PCT-US01-19110-1666	Sequence 1666, Ap
7	1147.5	88.3	252	22 US-09-880-748-1666	Sequence 1666, Ap

8	1139	87.6	253	1 PCT-US01-19110-1880	Sequence 1880, Ap
9	1139	87.6	253	22 US-09-880-748-1880	Sequence 1880, Ap
10	1136	87.4	251	1 PCT-US01-19110-1756	Sequence 1756, Ap
11	1136	87.4	251	22 US-09-880-748-1756	Sequence 1756, Ap
12	1133.5	87.2	254	1 PCT-US01-19110-1699	Sequence 1699, Ap
13	1133.5	87.2	254	22 US-09-880-748-1699	Sequence 1699, Ap
14	1130	86.9	247	1 PCT-US01-19110-1770	Sequence 1770, Ap
15	1130	86.9	247	22 US-09-880-748-1770	Sequence 1770, Ap
16	1129.5	86.9	254	1 PCT-US01-19110-1450	Sequence 1450, Ap
17	1129.5	86.9	254	22 US-09-880-748-1450	Sequence 1450, Ap
18	1128	86.8	247	1 PCT-US01-19110-1434	Sequence 1434, Ap
19	1128	86.8	247	22 US-09-880-748-1434	Sequence 1434, Ap
20	1128	86.8	247	22 US-09-880-748-1434	Sequence 1434, Ap
21	1128	86.8	247	22 US-09-880-748-1434	Sequence 1434, Ap
22	1126	86.6	251	1 PCT-US01-19110-1397	Sequence 1397, Ap
23	1126	86.6	251	22 US-09-880-748-1397	Sequence 1397, Ap
24	1124	86.5	247	1 PCT-US01-19110-1661	Sequence 1661, Ap
25	1124	86.5	247	22 US-09-880-748-1661	Sequence 1661, Ap
26	1123.5	86.4	250	1 PCT-US01-19110-947	Sequence 947, App
27	1123.5	86.4	250	22 US-09-880-748-947	Sequence 947, App
28	1121	86.2	247	1 PCT-US01-19110-1744	Sequence 1744, Ap
29	1121	86.2	247	22 US-09-880-748-1744	Sequence 1744, Ap
30	1120.5	86.2	246	1 PCT-US01-19110-1589	Sequence 1589, Ap
31	1120.5	86.2	246	22 US-09-880-748-1589	Sequence 1589, Ap
32	1116	85.8	247	1 PCT-US01-19110-1704	Sequence 1704, Ap
33	1116	85.8	247	22 US-09-880-748-1704	Sequence 1704, Ap
34	1115	85.8	245	1 PCT-US01-19110-846	Sequence 846, App
35	1115	85.8	245	1 PCT-US01-19110-1743	Sequence 1743, Ap
36	1115	85.8	245	22 US-09-880-748-846	Sequence 846, App
37	1115	85.8	245	22 US-09-880-748-1743	Sequence 1743, Ap
38	1115	85.8	249	1 PCT-US01-19110-1748	Sequence 1748, Ap
39	1115	85.8	249	22 US-09-880-748-1748	Sequence 1748, Ap
40	1114.5	85.7	250	1 PCT-US01-19110-1439	Sequence 1439, Ap
41	1114.5	85.7	250	1 PCT-US01-19110-1581	Sequence 1581, Ap
42	1114.5	85.7	250	22 US-09-880-748-1439	Sequence 1439, Ap
43	1114.5	85.7	250	22 US-09-880-748-1581	Sequence 1581, Ap
44	1113.5	85.7	252	1 PCT-US01-19110-1656	Sequence 1656, Ap
45	1113.5	85.7	252	22 US-09-880-748-1656	Sequence 1656, Ap

ALIGNMENTS

RESULT 1
US-08-779-457-49
; Sequence 49, Application US/08779457
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-779-457-49

Query Match 100.0%; Score 1300; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.9e-99;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCQSGGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
|||||
Db 1 EVQLVQSGAEVKKPGESLKISCQSGGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60

QY 61 AQKFQGRVTITADESTAYMELSSLRSEDTAVYICARDRVVVPATSLRGGMDVWGQTT 120
|||||
Db 61 AQKFQGRVTITADESTAYMELSSLRSEDTAVYICARDRVVVPATSLRGGMDVWGQTT 120

QY 121 VTVSSGGGGGGGGGSGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNVSWYQQ 180
|||||
Db 121 VTVSSGGGGGGGGGSGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNVSWYQQ 180

QY 181 HPGKAPKLMIEGSKRPSGVSNRFSGSKGSTASLTISGLQAEDEADYYCSSYTTRSTRV 240
|||||
Db 181 HPGKAPKLMIEGSKRPSGVSNRFSGSKGSTASLTISGLQAEDEADYYCSSYTTRSTRV 240

QY 241 FGGGTKLTVL 250
|||||
Db 241 FGGGTKLTVL 250

RESULT 2
PCT-US01-19110-1412
; Sequence 1412, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1412
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1412

Query Match 88.7%; Score 1152.5; DB 1; Length 254;

Best Local Similarity 87.4%; Pred. No. 1.1e-86;
Matches 221; Conservative 14; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCQSGGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||
Db 1 QVQLQQSGAEVKKPGSSVKVCKASGGTFFSSYAISWVRAPQGQLEWMGGIPIFGTANY 60

QY 61 AQKFQGRVTITADESTAYMELSSLRSEDTAVYICARD---RVVVPATSLRGGMDVWGQ 117
|||||
Db 61 AQKFQGRVTITADESTAYMELSLRSDDTAVYICARDGIYDILTTLVSYNGMDVWGK 120

QY 118 GTTQVTVSSGGGGGGGSGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNVSW 177
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Db 121 GTMVTVSSGGGGGGGSGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNVSW 180

QY 178 YQHPGKAPKLMIEGSKRPSGVSNRFSGSKGSTASLTISGLQAEDEADYYCSSYTTRS 237
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Db 181 YQHPGKAPKLMIEGSKRPSGVSNRFSGSKSGNTASLTISGLQAKDEADYYCSSYTTRS 240

QY 238 TRVFGGTTKLTVL 250
|||||
Db 241 TRVFGGTTKLTVL 253

RESULT 3
US-09-880-748-1412
; Sequence 1412, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1412
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1412

Query Match 88.7%; Score 1152.5; DB 22; Length 254;
Best Local Similarity 87.4%; Pred. No. 1.1e-86;
Matches 221; Conservative 14; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCQSGGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||
Db 1 QVQLQQSGAEVKKPGSSVKVCKASGGTFFSSYAISWVRAPQGQLEWMGGIPIFGTANY 60

QY 61 AQKFQGRVTITADESTAYMELSSLRSEDTAVYICARD---RVVVPATSLRGGMDVWGQ 117
|||||
Db 61 AQKFQGRVTITADESTAYMELSLRSDDTAVYICARDGIYDILTTLVSYNGMDVWGK 120

QY 118 GTTQVTVSSGGGGGGGSGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNVSW 177
|||
Db 121 GTMVTVSSGGGGGGGSGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNVSW 180

QY 178 YQHPGKAPKLMIEGSKRPSGVSNRFSGSKGSTASLTISGLQAEDEADYYCSSYTTRS 237
|||||
Db 181 YQHPGKAPKLMIEGSKRPSGVSNRFSGSKSGNTASLTISGLQAKDEADYYCSSYTTRS 240

QY 238 TRVFGGTTKLTVL 250

Db241TRVFGGGTKLTVL253

|||||

RESULT4

PCT-US01-19110-1813

; Sequence 1813, Application PC/TUS0119110

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Antibodies that immunospecifically Bind Blys

; FILE REFERENCE: PF523PCT

; CURRENT APPLICATION NUMBER: PCT/US01/19110

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1813

; LENGTH: 253

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US01-19110-1813

Query Match88.4%; Score 1149; DB 1; Length 253;

Best Local Similarity87.7%; Pred. No. 2e-86;

Matches 221; Conservative 13; Mismatches 16; Indels 2; Gaps 1;

QY1EVQLVQSGAEVKKPGESLKISCGSGGTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY60

|||||

Db1EVQLVQSGAEVKKPGSSVRVSKASGGTFSNYAINWVRQAPGQGLEWMGGIIPMGTTTRY60

|||||

QY61AQKFGQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRV--VVPATSLRGGMDVWGQ118

|||||

Db61AQKFGQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDGSDYDILTYGYYIDNYMDVWGGRG120

|||||

QY119TTVTVSSGGGGGGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNYVSWY178

|||||

Db121TLTVTSSGGGGGGGGSQSVLTQTPASVSGSPGQSITISCTGTSSDVGGYNYVSWY180

|||||

QY179QQHPGKAPKLMIEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTTRST238

|||||

Db181QQHPGKAPKLMIEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTTRST240

|||||

QY239RVFGGGTKLTVL250

|||||

Db241RVFGGGTKLTVL252

|||||

RESULT5

PCT-US01-19110-1666

; Sequence 1666, Application PC/TUS0119110

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523PCT

; CURRENT APPLICATION NUMBER: PCT/US01/19110

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1666

; LENGTH: 252

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US01-19110-1666

Query Match88.3%; Score 1147.5; DB 1; Length 252;

Best Local Similarity88.5%; Pred. No. 2.7e-86;

Matches 223; Conservative 13; Mismatches 13; Indels 3; Gaps 2;

QY1EVQLVQSGAEVKKPGESLKISCGSGGTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY60

|||||

Db1QVQLLSAAEVKKPGSSVKVSKASGGTFSSYKAIWVRQAPGQGLEWMGGIPIFGTANY60

|||||


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; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1699
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1699

Query Match      87.2%; Score 1133.5; DB 1; Length 254;
Best Local Similarity 87.0%; Pred. No. 3.9e-85;
Matches 220; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
   :||| ||||| ||| |::||| :||| ||||| :||| ||||| ||| | |||
Db 1 QVQLQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANY 60

QY 61 AQKFGGRVTITADESTSTAYMELSSLRSEDTAVYYCARD---RVVVPATSLRGGMDVWGQ 117
   ||||| ||||| ||| :||| ||||| ||||| ||||| :| :||| |||||
Db 61 AQKFGGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDYNYDILTGHPYYYGMDVWGR 120

QY 118 GTTVTVSSGGGGGGGGGSGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSW 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GTTVTVSSGGGGGGGGGSGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSW 180

QY 178 YQHPGKAPKLMIEGSKRPSGVNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTRSR 237
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 YQHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTRSR 240

QY 238 TRVFGGGTKLTVL 250
   ||||| ||||| |||
Db 241 TRVFGGGTKLTVL 253

RESULT 13
US-09-880-748-1699
; Sequence 1699, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1699
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1699

Query Match      87.2%; Score 1133.5; DB 22; Length 254;
Best Local Similarity 87.0%; Pred. No. 3.9e-85;
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```
Matches 220; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
   :||| ||||| ||| |::||| :||| ||||| :||| ||||| ||| | |||
Db 1 QVQLQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANY 60

QY 61 AQKFGGRVTITADESTSTAYMELSSLRSEDTAVYYCARD---RVVVPATSLRGGMDVWGQ 117
   ||||| ||||| ||| :||| ||||| ||||| ||||| :| :||| |||||
Db 61 AQKFGGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDYNYDILTGHPYYYGMDVWGR 120

QY 118 GTTVTVSSGGGGGGGGGSGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSW 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GTTVTVSSGGGGGGGGGSGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSW 180

QY 178 YQHPGKAPKLMIEGSKRPSGVNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTRSR 237
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 YQHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTRSR 240

QY 238 TRVFGGGTKLTVL 250
   ||||| ||||| |||
Db 241 TRVFGGGTKLTVL 253

RESULT 14
PCT-US01-19110-1770
; Sequence 1770, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1770
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1770

Query Match      86.9%; Score 1130; DB 1; Length 247;
Best Local Similarity 87.3%; Pred. No. 7.3e-85;
Matches 219; Conservative 12; Mismatches 14; Indels 6; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
   ||||| ||||| ||| :||| ||||| :||| ||||| ||| | |||
Db 1 EVQLVQSGAEVKKPGSSVKVCKTSGGTFSSYAISWVRQAPGQGLEWMGILPIFGPARY 60

QY 61 AQKFGGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRG-GMDVWGQGT 119
   |::||| ||||| | ||||| :||| ||||| ||| ||||| :|||
Db 61 AEKFGGRVTITADELTRTAYMELKTLRSDDTAVYYCAR-----AGTSLMNYGMDVWGRT 115

QY 120 TTVTVSSGGGGGGGGGSGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQ 179
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 LTVTVSSGGGGGGGGGSGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQ 175

QY 180 QHPGKAPKLMIEGSKRPSGVNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTRSTR 239
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 QHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTRSTR 235

QY 240 VFGGGGTKLTVL 250
   ||||| ||||| |||
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Db 236 VFGGGTKLTVL 246

RESULT 15

US-09-880-748-1770
; Sequence 1770, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1770
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1770

Query Match		86.9%	Score 1130;	DB 22;	Length 247;
Best Local Similarity		87.3%	Pred. No. 7.3e-85;		
Matches 219;		Conservative 12;	Mismatches 14;	Indels 6;	Gaps 2;
QY	1	EVQLVQSGAEVKKPGESLKIS	CGSGTFSSYKMNVVRQAPGK	GLEWMGGILPIFGTANY	60
Db	1	EVQLVQSGAEVKKPGSSVKV	CKTSGGTFSSYAISWVRQAP	GQGLEWMGGILPIFGPARY	60
QY	61	AQKFGQGRVTITADESTST	AYMELSSLRSEDTAVYYC	ARDRVVVPATSLRG-GMDV	WGQGT 119
Db	61	AEKFGQGRVTITADELTR	AYMELKTLRSDDTAVYYC	AR-----AGTSLMNYG	MDVWGRGT 115
QY	120	TVTVSSGGGGGGGGGGG	SGSQSVLTQPA	SVSGSPGQSITISCTGTSS	DVCGYNYVSWYQ 179
Db	116	LVTVSSGGGGGGGGGGG	SGSQSVLTQPA	SVSGSPGQSITISCTGTSS	DVCGYNYVSWYQ 175
QY	180	QHPGKAPKLMIEGSKRPS	GVSNRFGSKSGSTASLT	ISGLQAEDEADYCSSY	TRSTR 239
Db	176	QHPGKAPKLMIEGSKRPS	GVSNRFGSKSGKNTASLT	ISGLQAEDEADYCSSY	TRSTR 235
QY	240	VFGGGTKLTVL	250		
Db	236	VFGGGTKLTVL	246		

Search completed: August 15, 2002, 16:34:05
Job time: 765 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:24:03 ; Search time 101.13 Seconds
(without alignments)
274.582 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SSYTRSTRVFGGTKLTVL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
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19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1300	100.0	250	AAW24062	Human WSX receptor
2	1163	89.5	249	AAB36083	Recombinant human
3	926.5	71.3	244	AAV06718	Antibody 12E10 sin
4	926	71.2	245	AAB67618	Human leukocyte an
5	918	70.6	245	AAB67617	Human leukocyte an
6	907.5	69.8	239	AAB69603	Huntingtin intrabo
7	896.5	69.0	243	AAG65591	Anti-hEDRF antibod
8	892	68.6	249	AAV06713	Antibody 10F6 sing
9	879.5	67.7	304	AAG63634	Amino acid sequenc
10	879.5	67.7	304	AAG63639	Amino acid sequenc
11	865	66.5	245	AAB67619	Human leukocyte an

12	857	65.9	310	20	AAW83324	Single chain Apo-2
13	826.5	63.6	249	18	AAW24061	Human WSX receptor
14	826	63.5	245	22	AAB67621	Human leukocyte an
15	821	63.2	245	22	AAB67623	Human leukocyte an
16	818	62.9	245	22	AAB67622	Human leukocyte an
17	817	62.8	258	18	AAW08487	C6 human sfv antib
18	813.5	62.6	242	21	AAV15127	Anti-murine CTLA-4
19	810.5	62.3	240	21	AAV15124	Anti-murine CTLA-4
20	810.5	62.3	240	21	AAV15125	Internalising anti
21	809.5	62.3	246	21	AAV58235	Human SCFv2 agains
22	807	62.1	237	19	AAW49691	H6FXscFv(CEA6)trip
23	802.5	61.7	330	20	AAW94267	H6FXtripBscFv(CEA6
24	802.5	61.7	331	20	AAW94268	H6FXscFv(CEA6)trip
25	802.5	61.7	592	20	AAW94269	Anti-platelet glyc
26	801.5	61.7	242	21	AAV95209	Human SCFv1 agains
27	798.5	61.4	236	19	AAW49690	Anti-HIV-1 MAb 447
28	793.5	61.0	272	16	AAW80381	Amino acid sequenc
29	791.5	60.9	242	20	AAV21881	Anti-HIV-1 MAb 447
30	790.5	60.8	272	16	AAW80391	Anti-HIV-1 MAb 447
31	789.5	60.7	272	16	AAW80408	Anti-HIV-1 MAb 447
32	789.5	60.7	272	16	AAW80399	Anti-HIV-1 MAb 447
33	788.5	60.7	272	16	AAW80384	Anti-HIV-1 MAb 447
34	788.5	60.7	272	16	AAW80385	Anti-HIV-1 MAb 447
35	787.5	60.6	272	16	AAW80400	Anti-HIV-1 MAb 447
36	787.5	60.6	272	16	AAW80392	Anti-HIV-1 MAb 447
37	787.5	60.6	272	16	AAW80393	Anti-HIV-1 MAb 447
38	787.5	60.6	272	16	AAW80394	Anti-HIV-1 MAb 447
39	787.5	60.6	272	16	AAW80395	Anti-HIV-1 MAb 447
40	787.5	60.6	272	16	AAW80396	Anti-HIV-1 MAb 447
41	787.5	60.6	272	16	AAW80397	Anti-HIV-1 MAb 447
42	787.5	60.6	272	16	AAW80398	Anti-HIV-1 MAb 447
43	787.5	60.6	272	16	AAW80387	Anti-HIV-1 MAb 447
44	787.5	60.6	272	16	AAW80378	Anti-HIV-1 MAb 447
45	787.5	60.6	272	16	AAW80379	Anti-HIV-1 MAb 447

ALIGNMENTS

RESULT 1
AAW24062
ID AAW24062 standard; Protein; 250 AA.
XX
AC AAW24062;
XX
DT 17-MAR-1998 (first entry)
XX Human WSX receptor agonist antibody clone #4.
DE Human; WSX receptor; clone #4; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW Type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.
XX
OS Homo sapiens.
XX
PN WO9725425-A1.
XX
PD 17-JUL-1997.
XX
PF 07-JAN-1997; 97WO-US00325.
XX
PR 20-JUN-1996; 96US-0667197.
PR 08-JAN-1996; 96US-0585005.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX

```
DR WPI; 1997-372864/34.
XX
PT WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
XX
PS Example 14; Pages 121-122; 219pp; English.
XX
CC The present sequence is an agonist antibody clone to the human WSX
CC receptor, which can be used to identify and purify ligands and
CC activators. An anti-WSX receptor antibody can be used as an agonist
CC to activate the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. WSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 1300; DB 18; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
Db 1 evqlvqsgaevkkpgeslkiscqsgftfssykmnwvrqapgkglewmggiipifgtany 60

QY 61 AQKFQGRVTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQTT 120
Db 61 aqkfgrvtitadeststaymelsslrse dtavyycardrvvvpatslrggmdvwgqgtt 120

QY 121 VTVSSGGGGGGGGGGGSGSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQ 180
Db 121 vtvssggggggggggsgsvltqpasvsgspgqsitisctgtssdvvggynyvswyqq 180

QY 181 HPGKAPKLMIEGSKRPVSNRFSKSGSGTASLTISGLQAEDEADYYCSSYTRSTRV 240
Db 181 hpgkapklmiyegskrpvsnrfsksgsgtastltisglqaeadeadyyccsytrstrv 240

QY 241 FGGGTGKLTVL 250
Db 241 fgggtkltvl 250

RESULT 2
AAB36083
ID AAB36083 standard; Protein; 249 AA.
XX
AC AAB36083;
XX
DT 16-FEB-2001 (first entry)
XX
DE Recombinant human antibody scFv TN11.
XX
KW Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
KW cTN-C.
XX
OS Homo sapiens.
XX
PN WO200063699-A1.
XX
PD 26-OCT-2000.
```

```
XX 19-APR-2000; 2000WO-EP03550.
PF
XX 20-APR-1999; 99IT-FI00094.
PR
XX (PHIL-) PHILOGEN SRL.
PA
XX Zardi L;
PI
XX WPI; 2000-687225/67.
DR N-PSDB; AAC67868.
XX
PT Ligands used for diagnosis and treatment of human neoplasias, are
PT capable of identifying the tenascin-C isoform containing domain C of
PT tenascin-C -
XX
PS Disclosure; Page 5-6; 31pp; English.
XX
CC The present sequence is a recombinant human antibody scFv. Antibody
CC TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
CC recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
CC only capable of recognising TN-C isoforms containing domain C (cTN-C).
CC TN11 is useful for detecting the presence of TN-C isoforms in vitro or
CC in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C.
CC It is useful for the preparation of formulations for the treatment of
CC human neoplasias.
XX
SQ Sequence 249 AA;

Query Match 89.5%; Score 1163; DB 21; Length 249;
Best Local Similarity 89.6%; Pred. No. 2.3e-71;
Matches 225; Conservative 11; Mismatches 11; Indels 4; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
Db 1 evqlvqsgaevkkpgssvkysckasggtfssyaiswvrqapgqglewmggiipifgtany 60

QY 61 AQKFQGRVTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGT 119
Db 61 aqkfgrvtitadeststaymelsslrse dtavyycardrvvvpatslrggmdvwgqgt 117

QY 120 TVTVSSGGGGGGGGGGGSGSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQ 179
Db 118 mvtvssggggggggsgsvltqpasvsgspgqsitisctgtssdvvggynyvswyqq 177

QY 180 QHPGKAPKLMIEGSKRPVSNRFSKSGSGTASLTISGLQAEDEADYYCSSYTRSTR 239
Db 178 qhpgakplmiyegskrpvsnrfsksgsgtastltisglqaeadeadyyccsytrstr 237

QY 240 VFGGTGKLTVL 250
Db 238 vfgggtkltvl 248

RESULT 3
AAY06718
ID AAY06718 standard; Protein; 244 AA.
XX
AC AAY06718;
XX
DT 17-JUN-1999 (first entry)
XX
DE Antibody 12E10 single chain Fv (scFv) fragment.
XX
KW Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
KW megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MusK; CDR;
KW neuromuscular; muscular dystrophy; complementarity determining region.
XX
OS Homo sapiens.
XX
```



```
RESULT 5
AAB67617
ID AAB67617 standard; Protein; 245 AA.
XX AC AAB67617;
XX DT 29-MAY-2001 (first entry)
XX DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_1.
XX KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
XX KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
XX OS Homo sapiens.
XX PN WO200114558-A1.
XX PD 01-MAR-2001.
XX PF 28-AUG-2000; 2000WO-EP08388.
XX PR 26-AUG-1999; 99EP-0116691.
XX PA (MORP-) MORPHOSYS AG.
XX PI Kretzschmar T, Tesar M, Marget M, Kroenke M;
XX DR WPI; 2001-218451/22.
XX PT Novel isolated human immunoglobulin or functional immunoglobulin
PT fragment specific for human leukocyte antigen Cw6, useful for treatment
PT of humans and for human leukocyte antigen phenotyping -
XX PS Claim 3; Fig 1; 23pp; English.
XX CC AAB67617-23 represent single chain antibody (scFv) fragments which
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
CC derived from a synthetic human combinatorial antibody library based on
CC molecular consensus frameworks and CDRs randomised with trinucleotides.
CC The specification describes a human immunoglobulin fragments specific
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
CC studies of natural killer cell silencing as well as miscarriages.
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
CC fragments are useful for the preparation of a pharmaceutical for the
CC treatment of humans. They are also useful for HLA phenotyping.
XX SQ Sequence 245 AA;

Query Match 70.6%; Score 918; DB 22; Length 245;
Best Local Similarity 72.2%; Pred. NO. 8.1e-55;
Matches 184; Conservative 18; Mismatches 37; Indels 16; Gaps 3;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
Db 1 qvqlvqsgaevkkgssvkvscckasggtfssyaiswvrqapggglewmggiipfgtany 60
QY 61 AQKFQGRVTITADESTSTAYMELSSRLSRSEDVAVYICARDRVVVPATSLRGMDVWGQGT 120
Db 61 aqkfqgrvtitadeststaymelssrlsrse dtavvyicarydf-----syldywgqgtl 112
QY 121 VTVS-----SGGGGGGGGGGGSQSVLTQPASVSGSPGQSITISCTGTSDDVGGYNYV 175
Db 113 vtvssagggsgggsgggsgggsggdieltqpssvsvapgtariscsg---dalgdka 169
QY 176 SWYQQHPGKAPKLMIEGSKRPSGVSNRFGSKSGSTASLTISGLQAEDEADYVCSSYTT 235
Db 170 swyqqkpgqapvlvyddsdrrpsgiperfsgsgntatltisgtqaedeaddyccsydd 229
QY 236 RSTRVFGGGTKLTVL 250
Db 230 veavvfqggtkltl 244
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```
RESULT 6
AAB69603
ID AAB69603 standard; Protein; 239 AA.
XX AC AAB69603;
XX DT 30-APR-2001 (first entry)
XX DE Huntingtin intrabody alpha-Nt-HD-C4 sFv.
XX KW Neurological disorder; Huntington's disease; Alzheimer's disease;
KW Parkinson's disease; prion disease; frontotemporal dementia;
KW amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy;
KW dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1;
KW SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody.
XX OS Unidentified.
XX PN WO200106989-A2.
XX PD 01-FEB-2001.
XX PF 24-JUL-2000; 2000WO-US20131.
XX PR 27-JUL-1999; 99US-0146047.
XX PR 21-JUL-2000; 2000US-0620955.
XX PA (HUST/) HUSTON J S.
XX PA (MESS/) MESSER A.
XX PA (LECE/) LECERF J.
XX PI Huston JS, Messer A, Lecerf J;
XX DR WPI; 2001-182700/18.
XX DR N-PSDB; AAF58707.
XX PT Inhibiting intracellular polypeptide accumulation, useful for treating
PT neurological disorders, e.g. Alzheimer's disease, comprises contacting
PT the polypeptide with a specific intrabody -
XX PS Claim 22; Page 95; 108pp; English.
XX CC The present invention describes a method for inhibiting the formation of
CC aggregates of certain proteins, involving contacting the protein with a
CC binding molecule known as an intrabody. Proteins to be bound include
CC those associated with neurological disorders, and so the method can be
CC used in the prevention of diseases such as Alzheimer's, Parkinson's and
CC Huntington's diseases, prion disease, frontotemporal dementia,
CC amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy,
CC dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1
CC (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7.
XX SQ Sequence 239 AA;
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```
Query Match 69.8%; Score 907.5; DB 22; Length 239;
Best Local Similarity 70.0%; Pred. NO. 4.1e-54;
Matches 175; Conservative 26; Mismatches 38; Indels 11; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
Db 1 qvqlqesggglvqpqgslrlscaasgftfssysmswvrqapkglewavvisydgskyy 60
QY 61 AQKFQGRVTITADESTSTAYMELSSRLSRSEDVAVYICARDRVVVPATSLRGMDVWGQGT 120
Db 61 adsvkgrftisrdnsknltlylqmsnlraedtavyycardry-----fdlwgrgtl 110
QY 121 VTVSSGGGGGGGGGGSQSVLTQPASVSGSPGQSITISCTGTSDDVGGYNYVSWYQQ 180
Db 111 vtvssgggsgggsgggsggsgaltqpasvsgsgqstisctgtssldlgaynyvswyqq 170
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DR WPI; 2001-496986/54.
DR N-PSDB; AAH74679.
XX
PT Remedies for hepatitis C containing substances with antiviral effects
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT compounds, by inhibiting binding of hepatitis C virus envelope
PT glycoprotein or CD81
XX
PS Disclosure; Page 103-105; 138pp; Japanese.
PS
XX
CC The present sequence represents the H chain variable region of a single
CC chain antibody of the invention. The specification describes a substance
CC can inhibit the binding between hepatitis C virus (HCV) and cells with
CC potential HCV infection, cells with expression of CD81, or CD81. This
CC substance is especially an antibody with affinity towards HCV E2/NS1
CC protein, containing amino acid sequences based on the complementarity
CC determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable
CC regions. The antibody inhibits the viral envelope glycoprotein. It is
CC also a CD81 inhibitor. The antibodies and drugs are used for treatment
CC and/or prevention of hepatitis C, or for diagnosis of hepatitis C.
XX
SQ Sequence 304 AA;

Query Match 67.7%; Score 879.5; DB 22; Length 304;
Best Local Similarity 68.2%; Pred. No. 4e-52;
Matches 176; Conservative 32; Mismatches 37; Indels 13; Gaps 6;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
Db 23 evqlvesgaevkpssvkvsckasggtlydqplgwvrqapggglewmggilplsgpphy 82
QY 61 AQKFQGRVTITADESTSTAYMELSSLRSEDVAVYICARDRVVVPATSLRGG---MDVWG 116
Db 83 aqkfqgkvsitadeststayleltstsedtavyycar--vlgrycrrgscydwldpwg 139
QY 117 QGTTVTVSSGGGGGGGGGGGS--QSVLTQPASVSGSPGQSITISCTGSSDVG-GYN 173
Db 140 qgtlvtvssggsgggsgggsgggsgalqavltqpsvsgppgqrvtisctgssnigayd 199
QY 174 YVSWYQQHPGKAPKLMIEGSKRPSGVSNRFGSGKSGSTASLTISGLQAEDEADYYCSSY 233
Db 200 -vhwyqqlpgtapklllygnnrpsgvdpdrfsgkskgsaslaigtlgadeadeayycsy 258
QY 234 TTRST--RVFEGGKTLTV 249
Db 259 dsslsgefvgfgtgkvei 276

RESULT 11
AAB67619
ID AAB67619 standard; Protein; 245 AA.
XX
AC AAB67619;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_3.
XX
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
XX
OS Homo sapiens.
XX
PN WO200114558-A1.
XX
PD 01-MAR-2001.
XX
PF 28-AUG-2000; 2000WO-EP08388.
XX
PR 26-AUG-1999; 99EP-0116691.
XX
PA (MORP-) MORPHOSYS AG.

XX Kretzschmar T, Tesar M, Marget M, Kroenke M;
XX WPI; 2001-218451/22.
DR
XX
PT Novel isolated human immunoglobulin or functional immunoglobulin
PT fragment specific for human leukocyte antigen Cw6, useful for treatment
PT of humans and for human leukocyte antigen phenotyping
XX
PS Claim 3; Fig 1; 23pp; English.
PS
XX
CC AAB67617-23 represent single chain antibody (scFv) fragments which
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
CC derived from a synthetic human combinatorial antibody library based on
CC molecular consensus frameworks and CDRs randomised with trinucleotides.
CC The specification describes a human immunoglobulin fragments specific
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
CC studies of natural killer cell silencing as well as miscarriages.
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
CC fragments are useful for the preparation of a pharmaceutical for the
CC treatment of humans. They are also useful for HLA phenotyping.
XX
SQ Sequence 245 AA;

Query Match 66.5%; Score 865; DB 22; Length 245;
Best Local Similarity 68.6%; Pred. No. 3.1e-51;
Matches 175; Conservative 18; Mismatches 46; Indels 16; Gaps 3;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
Db 1 qvqlvsgaevkpssvkvsckasgytftsyyhmhwrqapggglewmgwlnpsggtny 60
QY 61 AQKFQGRVTITADESTSTAYMELSSLRSEDVAVYICARDRVVVPATSLRGGMDVWGQGT 120
Db 61 aqkfgrvtmtrdtsistaymelsslrsestavyycargsf-----dfmdnwgqgtl 112
QY 121 VTVS-----SGGGGGGGGGGGSGSVLTQPASVSGSPGQSITISCTGSSDVGGYNYV 175
Db 113 vtvssagggsgggsgggsgggsgdieltqppsvsavgqtariscg---dalqdkya 169
QY 176 SWYQQHPGKAPKLMIEGSKRPSGVSNRFGSGKSGSTASLTISGLQAEDEADYYCSSYTT 235
Db 170 swyqqkpgqapvlviyddsdprpsgiperfsgsngntatltisgtqaedeadeayycsydd 229
QY 236 RSTRVFGGGTKLTVL 250
Db 230 tdlivfgggtkltlv 244

RESULT 12
AAW83324
ID AAW83324 standard; Protein; 310 AA.
XX
AC AAW83324;
XX
DT 16-MAR-1999 (first entry)
XX
DE Single chain Apo-2 antibody 24C4.
XX
KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW TNF cytokine.
XX
OS Homo sapiens;
XX
PN WO9851793-A1.
XX
PD 19-NOV-1998.
XX
PF 14-MAY-1998; 98WO-US09704.
XX
```

```
PR 09-FEB-1998; 98US-0020746.
PR 15-MAY-1997; 97US-0857216.
XX (GETH ) GENENTECH INC.
PA Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
PI
XX
XX WPI; 1999-045228/04.
DR N-PSDB; AAV72534.
XX
PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
PT conditions linked with decreased apoptosis e.g. cancer, and produce
PT antibodies to increase or decrease apoptosis
XX
PS Example 14; Fig 16; 134pp; English.
XX
CC The present invention describes human Apo-2. Apo-2 can be used
CC therapeutically to induce apoptosis in mammalian cells, and so is useful
CC to treat conditions associated with decreased apoptosis e.g. cancer.
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
CC can be used to identify agents activating Apo-2, useful to treat
CC mammalian cancer cells, and to produce Apo-2 chimeras useful
CC therapeutically (e.g. those containing immunoglobulin sequences can be
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
CC tag polypeptide allow Apo-2 detection and purification using anti-tag
CC antibodies). It can be used to produce antibodies which can be combined
CC with a (particularly pharmaceutically acceptable) carrier in compositions
CC or used to produce dimeric molecules (especially homodimeric molecules
CC comprising first and second Apo-2 antibodies). Agonistic (especially
CC single-chain) antibodies can be administered to induce apoptosis in
CC mammalian cancer cells, and antagonistic antibodies used to block
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
CC antibodies may also be used diagnostically e.g. to detect Apo-2
CC expression in cells/tissues and in Apo-2 purification. The present
CC sequence represents a single chain Apo-2 antibody, designated 24C4.
XX
SQ Sequence 310 AA;

Query Match 65.9%; Score 857; DB 20; Length 310;
Best Local Similarity 66.7%; Pred. No. 1.4e-50;
Matches 170; Conservative 29; Mismatches 40; Indels 16; Gaps 4;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
Db :||||| | :|| ||: || ||| ||| | ||| ||| ||| ||| : || |
40 qvqlvsgggvvqpgrslrlscaasgfifssygmhvwvrqapgkglewvagifydggnkyy 99
QY 61 AQKFGQGRVTITADESTSTAYNELSSLRSEDATVYYCARDRVVVPATSLRGG---MDVWGQ 117
Db | :|| ||: | | :| :||| :||| ||| ||| ||| ||| | ||| :
100 adsvkgrftlsrdnsknltlylqmslraedtavyycardr-----gyyyymdvwgk 149

QY 118 GTTWTVSSGGGGGGGGGSGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSW 177
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||
150 gttvtvssggggsgggsggsgsvltqpssvsgapgrvtlsctgrssnlgaghdvhw 209

QY 178 YQHPGKAPKLMIEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYVCSSYTRS 237
Db || | ||| :|| : |||| :||| :||| :||| :||| :||| :||| :|| : |
210 yqqlpgtapklllyddsnrpsgvpdrfsgsrsgtsaslaigtqlqaeadayycqsyds-s 268

QY 238 TR--VFGGGTKLTVL 250
Db | ||||| :|||
269 lrgsvfgggtkvtvl 283

RESULT 13
AAW24061
ID AAW24061 standard; Protein; 249 AA.
XX
AC AAW24061;
XX
DT 17-MAR-1998 (first entry)
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XX DE Human WSX receptor agonist antibody clone #3.
XX KW Human; WSX receptor; clone #3; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW Type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.
XX OS Homo sapiens.
XX PN WO9725425-A1.
XX 17-JUL-1997.
XX 07-JAN-1997; 97WO-US00325.
XX 20-JUN-1996; 96US-0667197.
PR 08-JAN-1996; 96US-0585005.
XX (GETH ) GENENTECH INC.
XX Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX WPI; 1997-372864/34.
XX WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
XX
PS Example 14; Pages 120-121; 219pp; English.
XX The present sequence is an agonist antibody clone to the human WSX
CC receptor, which can be used to identify and purify ligands and
CC activators. An anti-WSX receptor antibody can be used as an agonist
CC to activate the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. WSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
XX SQ Sequence 249 AA;
```

```
Query Match 63.6%; Score 826.5; DB 18; Length 249;
Best Local Similarity 66.8%; Pred. No. 1.3e-48;
Matches 169; Conservative 26; Mismatches 51; Indels 7; Gaps 5;
```

```
QY 1 EVQLVQSGAEVKKPGESLKISCGSGGFTFSSYKMNWVRQAPGKGLEWMGGIIPFGTANY 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||
1 evqlvqsgaevkkpgasvkvscasgyftgyymyvrqapggglewmgwinpnsqgtny 60

QY 61 AQKFGQGRVTITADESTSTAYNELSSLRSEDATVYYCARDRVVVPATSLRGG--MDVWGQ 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || ||||| |
61 aqkfggrvtmtrdtsigtaymelsrlssddtavyycardryygssayhrsgymdvwgrg 120

QY 119 TTVTVSSGGGGGGGGGSGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWY 178
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| : | |||
121 tlvtvssggggtggsgsgsgs-seltqdpavsalggtvritcqqds--lrsy-yaswy 176
```


Qy 121 VTVS-----SGGGGGGGGGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYV 175
Db 113 vtvssagggsgggsgggsgggdieltqppsvsvapqqtariscsg---dalgdkya 169
Qy 176 SWYQHPGKAPKLMIEGSKRPSGVSNRFGSKSGSTASLTISGLQAEDEADYVCSSYTT 235
Db 170 swyqqkpgqapvlviyddsdrrpsgiperfsgnsngntatltisgtqaedeaddyccsydy 229
Qy 236 RSTRVFGGTTKLTVL 250
Db 230 frdvvf9ggtklctl 244

Search completed: August 15, 2002, 16:24:04
Job time: 314 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:36:09 ; Search time 28.14 Seconds
(without alignments)
343.990 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKKPGESLK.....SSYTRSTRVFGGKLTVL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	506	38.9	111	1	LV2B_HUMAN
2	494.5	38.0	112	1	LV2K_HUMAN
3	469	36.1	111	1	LV2H_HUMAN
4	462	35.5	111	1	LV2D_HUMAN
5	457	35.2	111	1	LV2F_HUMAN
6	454	34.9	111	1	LV2C_HUMAN
7	452	34.8	111	1	LV2G_HUMAN
8	451	34.7	111	1	LV2A_HUMAN
9	435	33.5	109	1	LV2E_HUMAN
10	430	33.1	111	1	LV2I_HUMAN
11	420	32.3	117	1	HV1A_HUMAN
12	411.5	31.7	110	1	LV2J_HUMAN
13	401	30.8	117	1	HV1B_HUMAN
14	385	29.6	130	1	LV1G_HUMAN
15	384	29.5	117	1	HV1G_HUMAN
16	380.5	29.3	112	1	LV1B_HUMAN
17	380	29.2	117	1	HV13_MOUSE
18	378.5	29.1	147	1	HV1C_HUMAN
19	375	28.8	111	1	LV1D_HUMAN
20	374	28.8	109	1	LV1F_HUMAN
21	372.5	28.7	114	1	HV00_MOUSE
22	372.5	28.7	118	1	HV51_MOUSE
23	372	28.6	117	1	HV12_MOUSE
24	371	28.5	103	1	LV1E_HUMAN
25	367	28.2	140	1	HV02_MOUSE
26	365.5	28.1	120	1	HV50_MOUSE
27	365	28.1	111	1	LV2L_HUMAN
28	362.5	27.9	139	1	HV07_MOUSE
29	361.5	27.8	137	1	HV11_MOUSE
30	361	27.8	120	1	HV03_MOUSE
31	353	27.2	111	1	LV1A_HUMAN
32	353	27.2	111	1	LV1C_HUMAN
33	351	27.0	109	1	LV1I_HUMAN

34	347.5	26.7	112	1	LV1H_HUMAN	P06887	homo sapien
35	345	26.5	111	1	LV6C_HUMAN	P06317	homo sapien
36	345	26.5	121	1	HV01_MOUSE	P01745	mus musculus
37	344	26.5	106	1	LV4E_HUMAN	P06889	homo sapien
38	344	26.5	121	1	HV3J_HUMAN	P01771	homo sapien
39	338.5	26.0	122	1	HV3G_HUMAN	P01768	homo sapien
40	338	26.0	111	1	LV6D_HUMAN	P06318	homo sapien
41	337.5	26.0	119	1	HV38_MOUSE	P01808	mus musculus
42	336.5	25.9	122	1	HV3H_HUMAN	P01769	homo sapien
43	334.5	25.7	112	1	LV6A_HUMAN	P01721	homo sapien
44	334.5	25.7	131	1	LV6E_HUMAN	P06319	homo sapien
45	334	25.7	125	1	HV1F_HUMAN	P06326	homo sapien

ALIGNMENTS

RESULT 1
LV2B_HUMAN
ID LV2B_HUMAN STANDARD; PRT; 111 AA.
AC P01705;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region NEI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72233223; PubMed=5043326;
RA Garver F.A., Hilschmann N.;
RT "The primary structure of a monoclonal human lambda-type
immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL Eur. J. Biochem. 26:10-32(1972).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01970; L2HUNI.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Glycoprotein.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .).
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

Query Match 38.9%; Score 506; DB 1; Length 111;
Best Local Similarity 87.3%; Pred. No. 1.1e-28;
Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 141 QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYEGSKRPSGV 200
|| |||||
Db 1 QSALTQPASVSGSPGQSITISCTGTSDVGSYNFVSWYQQNPGKAPKLMYEGNKRPSPGV 60

QY 201 SNRFGSKSGSTASLTISGLQAEADYVCSYTRSTRVFGGKLTVL 250
|||||
Db 61 SNRFGSKSGKSTASLTISGLQVEADYVCSYAGNSTRVFGGKTRTVL 110

RESULT 2
LV2K_HUMAN
ID LV2K_HUMAN STANDARD; PRT; 112 AA.
AC P04209;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region NIG-84.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85204383; PubMed=3922791;
RA Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT myeloma-associated systemic amyloidosis."
RL FEBS Lett. 185:139-141(1985).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
CC INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
DR PIR; A01971; L2HUNG.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;

Query Match 38.0%; Score 494.5; DB 1; Length 112;
Best Local Similarity 84.7%; Pred. No. 6.6e-28;
Matches 94; Conservative 12; Mismatches 4; Indels 1; Gaps 1;

QY 141 QSVLTQPASVSGSPQSITISCTGTSSDVGGYVSWYQQHPGKAPKLMIEGSKRPSGV 200
Db 1 QSALTQPASVSGSPQSITISCTGTSSDVGGYVSWYQQHPGKAPKLLIYDVNSRPSGI 60

QY 201 SNRFGSKSGSTASLTISGLQAEDEADYYCSTYTRSTR-VFSGGKLTVL 250
Db 61 SNRFGSKSGNTASLTISGLQAEDEADYYCSTFTTNSRAVFGGKLTSLVL 111

RESULT 3
LV2H_HUMAN STANDARD; PRT; 111 AA.
AC P01711;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region VII.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71215142; PubMed=5087637;
RA Ponstingl H., Hilschmann N.;
RT "Structural rule of antibodies. Complete primary structure of a
RT monoclonal immunoglobulin L chain of the lambda type, subgroup II
RT (Bence Jones protein VII).";
RL Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01977; L2HUVL.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11445 MW; 3913736B3EF367E0 CRC64;

Query Match 36.1%; Score 469; DB 1; Length 111;
Best Local Similarity 84.4%; Pred. No. 3.7e-26;
Matches 92; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
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QY 142 SVLTQPASVSGSPQSITISCTGTSSDVGGYVSWYQQHPGKAPKLMIEGSKRPSGV 201
Db 2 SALTQPASVSGSLQSQSITISCTGTSSDVGGYVSWFQQHPGTAPKLIIEVNRPSGV 61
RP SEQUENCE.
QY 202 NREFSGSKSGSTASLTISGLQAEDEADYYCSTYTRSTRVFSGGKLTVL 250
Db 62 DREFSGKSANTASLTISGLQAEDEADYYCSTYSSNSVVFSGGKLTVL 110

RESULT 4
LV2D_HUMAN STANDARD; PRT; 111 AA.
AC P01707;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region TRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80114123; PubMed=118915;
RA Scholz R., Yang C., Hilschmann N.;
RT "Rule of antibody structure. Primary structure of a human monoclonal
RT IgA1-immunoglobulin (myeloma protein Tro). VI. Amino acid sequence of
RT the L-chain, lambda-type, subgroup II.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:1903-1918(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01973; L2HUTR.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11561 MW; 99DC457A12E8F6E1 CRC64;

Query Match 35.5%; Score 462; DB 1; Length 111;
Best Local Similarity 80.0%; Pred. No. 1.1e-25;
Matches 88; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 141 QSVLTQPASVSGSPQSITISCTGTSSDVGGYVSWYQQHPGKAPKLMIEGSKRPSGV 200
Db 1 QSALTQPRSVSGSPQSITISCTGTSSDVGGYVSWYQQHPGKAPKLMIFDVTKRPSGV 60
RP SEQUENCE.
QY 201 SNRFGSKSGSTASLTISGLQAEDEADYYCSTYTRSTRVFSGGKLTVL 250
Db 61 PDRLSGSKSGDTASLTISGLRADDEADYYCCSYAGRYSVIFGGGKLTVL 110

RESULT 5
LV2F_HUMAN STANDARD; PRT; 111 AA.
AC P01709;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region MGC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75013804; PubMed=4415202;
RA Fett J.W., Deutsch H.F.;
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Query Match      33.0%; Score 429; DB 4; Length 125;
Best Local Similarity 66.4%; Pred. No. 1.3e-25;
Matches 83; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGAEVKKPGASVKVCKASGYTFGYMHVVRQAPGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQGRVTITADESTSTAYMELSSLRSEDYAVYICARDRVVVPATSLRGGMDVWGQTT 120
   ||| |||||:| : ||||| ||||| ||||| ||||| : ||||| : |||||
Db 61 AQKVQGRVTMTFRDITISTAYMELSLRSDDTAVYICARSQGGGRIAAAGDAFDIWGQGT 120

QY 121 VTVSS 125
   |||||
Db 121 VTVSS 125

RESULT 8
Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL: AF240167; AAK43732.1; -.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match      33.0%; Score 428.5; DB 11; Length 170;
Best Local Similarity 53.8%; Pred. No. 2.1e-25;
Matches 85; Conservative 23; Mismatches 31; Indels 19; Gaps 3;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
   :|:| ||| || :|||:||||:||||:| |:|:| :|||:| | | | |
Db 3 QVKLQSGPEVVRPGVSVKISCKSGYTFDYSMHLKMNHAQSLEWIGIISTYDGNTNY 62

QY 61 AQKFGQGRVTITADESTSTAYMELSSLRSEDYAVYICARDRVVVPATSLRGG---MDVWGQ 117
   |||:| :| :|:| :|:|:| :|:|:|:| :|:|:|:| :| :| | |
Db 63 NQKFKGKATMTVRDKSSITAYMELARLTSDDSAIYYCARG-----AYYGSFYFDYWGQ 115

QY 118 GTTVTVSSGGSGGGGGGGSQSVLTQPAVSVSGSPG 155
   ||||| ||||| ||||| ||||| :
Db 116 GTTVTVSSGGSGGGGGGGGSE-----SSSPG 144

RESULT 9
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
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DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match      32.9%; Score 428; DB 4; Length 119;
Best Local Similarity 66.7%; Pred. No. 1.5e-25;
Matches 86; Conservative 11; Mismatches 18; Indels 14; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
   |||||:|||||:| |:|:| :|:|:| :|:|:|:|:|:|:|:|:| | | |
Db 1 EVQLVESGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPNSWTTNY 60

QY 61 AQKFGQGRVTITADESTSTAYMELSSLRSEDYAVYICARDRVVVPATSLRGG----MDVWG 116
   |||||:| |:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:| | | |
Db 61 AQKFGQKVTMTKDTISISTAYMELSLRSDDTAVYICARG-----GGRGLWFDPWG 110

QY 117 QGTTVTVSS 125
   ||| |||||
Db 111 QGTLVTVSS 119

RESULT 10
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL: BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match      32.9%; Score 428; DB 4; Length 614;
Best Local Similarity 32.0%; Pred. No. 1e-24;
Matches 122; Conservative 31; Mismatches 82; Indels 146; Gaps 12;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
   :|:| ||||| || :|:|:| :|:|:| :|:|:|:|:|:|:|:|:| | | |
Db 20 QMQLVQSGAEVKKPGSSVKVCKASGYTFTYRLHWVRQAPGQALEWMGWITPFNGNTNY 79

QY 61 AQKFGQGRVTITADESTSTAYMELSSLRSEDYAVYICARDRVVVPATSLRGGMDVWGQTT 120
   ||||| ||||| | | :||||| ||||| ||||| :| | | | | | | |
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SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match      37.0%; Score 491.5; DB 4; Length 124;
Best Local Similarity 75.8%; Pred. No. 6.1e-33;
Matches 97; Conservative 9; Mismatches 17; Indels 5; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESAEVKKPGASVKVSCKASGYTFSSYMHVVRQAPGQGLEWMGIINPSGGSTSY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSLSSDDTAVYYCARDRY-YGSSAYHRGSYYMDVWGR 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFQGRVTMTTRDTSSTVYMELSLRSDDTAVYYCARGLYVVVPAAFSR----FDYWGQ 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 GTLVTVSS 127
   |||||
Db 117 GTLVTVSS 124
   |||||

RESULT 8
Q96QS0
ID Q96QS0 PRELIMINARY; PRT; 159 AA.
AC Q96QS0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE MATRIX CELL ADHESION MOLECULE-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfilbrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match      36.1%; Score 479.5; DB 4; Length 159;
Best Local Similarity 72.5%; Pred. No. 7.8e-32;
Matches 95; Conservative 11; Mismatches 20; Indels 5; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTNYMNVVRQAPGQGPENWGINPNSGGSARY 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSLSSDDTAVYYCARDR--YYGSSAYHRGSYY--MDV 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SQKFQGRLTMTTRDTSSTVYMDLSLRSDDTAVYFCAREMEITFG-GAVSKGFYYGMDV 138
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 WGRGTLTVSS 127
   |||||
Db 139 WGQGTTVTVSS 149
   |||||

RESULT 9
Q925S2
ID Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

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RC STRAIN-BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match      36.0%; Score 479; DB 11; Length 170;
Best Local Similarity 63.4%; Pred. No. 9.3e-32;
Matches 90; Conservative 17; Mismatches 29; Indels 6; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVKLQSGPEVVRPGSVKISKSGGYTFDTYSMHVWLMKNHAQSLWIGLIISTYDGTNY 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYYMDVWGR 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 NQKFKGKATMTVDKSSITAYMELARLTSDSDSAIYGCARGAYYS-----FYFDYWGQ 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 TLTVSSGGGTGGGGGGGS 142
   | |||||:|||||:|||||
Db 117 TTVTVSSGGGGGGGGGGGS 138
   | |||||:|||||:|||||

RESULT 10
Q96GA6
ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAK09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match      35.0%; Score 465.5; DB 4; Length 614;
Best Local Similarity 44.6%; Pred. No. 5.5e-30;
Matches 112; Conservative 23; Mismatches 67; Indels 49; Gaps 9;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QMQLVQSGAEVKKPGSSVKVSCKASGYTFYRVLHWVRQAPGQALEWMGWITPFNGTNY 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSS---AYHRGSYYMDVW 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AQKFQDRVTITRDRSMNTAYMELSLRSDDTAMYYCARG--YSSSWDDAF-----DIW 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 GRGTLTVSSGGGTGGGGGGGSSELTQDPAYVALG----QTVRITCQDLSL--RSY 171
   |:||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 131 GQGTMVTVSS-----GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSI 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 172 YASWYQQKPGQAPVLIYVKNN----RPSGIPDRFSGSSSGNTASLTITGAQAEADYY 227
```

```
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 41.1%; Score 546; DB 4; Length 107;
Best Local Similarity 98.1%; Pred. No. 1.8e-37;
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 144 ELTQDPAVSVALGQTVRITCQGSLSRSYASWYQKPGQAPVLVIYGKNNRPSGIPDRFS 203
Db 1 ELTQDPVVSVALGQTVRITCQGSLSRSYASWYQKPGQAPVLVIYGKNNRPSGIPDRFS 60

QY 204 GSSSGNTASLTITGAQAEDEADYYCNSRDSNGHVVFGGTKLTVL 249
Db 61 GSSSGNTASLTITGAQAEDEADYYCNSRDSNGHNAVFGGTKLTVL 106

RESULT 5
Q9UL95
ID Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 41.1%; Score 546; DB 4; Length 125;
Best Local Similarity 81.9%; Pred. No. 2.2e-37;
Matches 104; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSRSLSSDDTAVYYCARDRIYRGSSAYHRGSYYMDVWGRG 120
Db 61 AQKVQGRVTMTTRDTSIGTAYMELSRSLSSDDTAVYYCARSGGGRIAAAGDAF--DIWQGG 118

QY 121 TLVTVSS 127
Db 119 TMVTVSS 125

RESULT 6
Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TReMBLrel. 13, Created).
```

```
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 39.8%; Score 529; DB 4; Length 119;
Best Local Similarity 81.9%; Pred. No. 5e-36;
Matches 104; Conservative 7; Mismatches 8; Indels 8; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPNSWTNY 60

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSRSLSSDDTAVYYCARDRIYRGSSAYHRGSYYMDVWGRG 120
Db 61 AQKFQGRVTMTKDTTSISTAYMELSRSLSSDDTAVYYCAR---GGG---RGLWF-DPWGQG 112

QY 121 TLVTVSS 127
Db 113 TLVTVSS 119

RESULT 7
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 124
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 16:35:35 ; Search time 91.6 Seconds
(without alignments)
470.259 Million cell up

Title: US-08-779-457-48
Perfect score: 1329
Sequence: 1 EVQLVQSGAEVKKPGASVKV.....SRDSSGNHVVFGGPKLTVL 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 5622222

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*
```

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	647.5	48.7	298	11	Q9QYF0	Q9qyf0 mus musculu
2	643	48.4	241	11	Q921A6	Q921a6 mus musculu
3	566.5	42.6	218	11	Q925S1	Q925s1 mus musculu
4	546	41.1	107	4	Q9NSD6	Q9nsd6 homo sapien
5	546	41.1	125	4	Q9UL95	Q9ul95 homo sapien
6	529	39.8	119	4	Q9UL94	Q9ul94 homo sapien
7	491.5	37.0	124	4	Q9UL92	Q9ul92 homo sapien
8	479.5	36.1	159	4	Q96QS0	Q96qs0 homo sapien
9	479	36.0	170	11	Q925S2	Q925s2 mus musculu
10	465.5	35.0	614	4	Q96GA6	Q96ga6 homo sapien
11	450.5	33.9	500	4	Q9BRV0	Q9brv0 homo sapien
12	450	33.9	119	5	Q9GYZ2	Q9gyz2 schistosoma
13	433	32.6	117	11	Q9QXE9	Q9qxe9 mus musculu
14	431	32.4	146	11	Q924R8	Q924r8 mus musculu
15	429.5	32.3	145	11	Q924Q7	Q924q7 mus musculu
16	425	32.0	146	11	Q924Q3	Q924q3 mus musculu

ALIGNMENTS

RESULT	1
Q9QYF0	
ID	PRELIMINARY; PRT; 298 AA.
AC	Q9QYF0
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Query Match 48.7%; Score 647.5; DB 11; Length 298;
Best Local Similarity 50.2%; Pred. No. 3.1e-45;
Matches 128; Conservative 36; Mismatches 68; Indels 23; Gaps 5;

QY	1	EVQLVQSGAEVKKPGASVKVSCKASGYTFITGYMYWVRQAPGGGLEWMGWINPNSGCTNY	60
	:	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	40	QVKLQQSGGGLVKPGGSLKLSCAASGDSFTRYMMSWVRQAPGKGLEWIGEINPDSSITYN	99

Search completed: August 15, 2002, 16:24:03
Job time: 313 sec

PS Disclosure; Fig 5; 89pp; English.

XX The present sequence is that of human single chain antibody (scFv)

CC H1b-1, which is directed against platelet glycoprotein Ib (GPIb).

CC H1b-1 is composed of a heavy chain variable region (see AAY95189)

CC and light chain variable region (see AAY95194) joined via a peptide

CC linker. The H1b series of scFv was isolated from a human synthetic

CC VH and VL scFv library by 3 rounds of phagemid selection against

CC transfect CHO cells expressing the GPIb alpha component of the

CC GPIb/IX/V complex on their surface, followed by a 4th round of

CC selection against washed human platelets, and 2 final rounds in

CC which attempts were made to displace scFv from washed platelets by

CC flooding with murine monoclonal antibody or mimotope peptide (see

CC AAY95229). Whether displayed as surface proteins on a phagemid or

CC secreted as free scFv by Escherichia coli, the H1b scFv clones are

CC capable of inhibiting von Willebrand factor-dependent aggregation of

CC platelets. The scFv are composed of native human protein sequences

CC and are therefore attractive potential reagents for therapeutic

CC purposes. They provide a new class of antithrombotic agents,

CC useful for the prevention of platelet-dependent thrombi in

CC diseased arteries, bypass grafts, dialysis etc., and can also be

CC used as diagnostic reagents. Methods of inhibiting aggregation

CC of platelets, of binding human platelet GPIb alpha and of selecting

CC a VH or VL region of an antibody that inhibits platelet aggregation

CC are claimed.

XX

SQ Sequence 238 AA;

Query Match 69.5%; Score 924; DB 21; Length 238;

Best Local Similarity 72.4%; Pred. No. 5e-55;

Matches 181; Conservative 22; Mismatches 33; Indels 14; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60

|||||:| | :|| |::|| ||||| | | |||||:||||: || | | |

Db 1 evqlvesggvvrpggslrlscaasgftddygmswvrqapgkglewvsginwngstgy 60

QY 61 AQKFQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAYHRGSYYMDVWGRG 120

| :|| |::|| : |::: | :|| ||||| : |

Db 61 adsvkgrftisrdnaknsllylqmnsraedtavyycaulk-----mphawgqg 108

QY 121 TLVTVSSGGGTGGGGGGG-SSELTQDPAVSVALGQTVRITCQGDSLRSYASWYQOK 179

|||||:| | ||||| | |||||:||||: |||||:||||: |||||: |||||

Db 109 tlvtvssgggsgggsggsalseltqdpavsalgtvritcqdslrsyyaswyqqk 168

QY 180 PGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVV 239

|||||:| | ||||| | |||||:||||: |||||:||||: |||||: |||||

Db 169 pgqapvlviygnknrrpsgipdrpsgssgntasltitgaqaedeaddyynsrdsngnh-v 227

QY 240 FGGGTKLTVL 249

|||||

Db 228 fgggktltvl 237

RESULT 15

AAB46055

ID AAB46055 standard; Peptide; 236 AA.

XX

AC AAB46055;

XX

DT 23-MAR-2001 (first entry)

XX

DE Human TF anti-idiotypic antibody fragment K9+.

XX

KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;

KW antidiotopic antibody; cytostatic; virucidal; antibacterial; TF antigen;

KW antiparasitic; infectious disease.

XX

OS Homo sapiens.

XX

PN WO2000073430-A2.

XX

PD 07-DEC-2000.

XX 29-MAY-2000; 2000WO-DE01809.

XX

XX 27-MAY-1999; 99DE-1024405.

PR 09-SEP-1999; 99DE-1043016.

XX

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX

XX Goletz S, Karsten U;

PI WPI; 2001-049937/06.

XX

XX Vaccines against conformation-dependent or non-peptide antigens, based

PT on DNA encoding peptide which mimics the antigen, useful e.g. as

PT antitumor vaccines -

XX

PS Disclosure; Page 13; 36pp; German.

XX

CC This invention describes a novel vaccine (V1) against

CC conformation-dependent antigens (CDA) comprising DNA (I) and/or an

CC antibody, or peptide which immunologically imitates CDA, is new. (I)

CC encodes a region of an antidiotopic antibody (Ab2) or another peptide

CC which: (a) specifically binds to the binding site of an antibody (Ab1)

CC or an antigen binding molecule; and (b) immunologically mimics the

CC initial antigen. The epitope is partially or completely

CC conformation-dependent, and has an immunogenic structure defined by a

CC specific spatial conformation of amino acids. (I) is used in the form

CC of linear or circular naked DNA and/or with a viral vector and/or

CC adjuvants. The products of the invention have cytostatic, virucidal,

CC antibacterial and antiparasitic. The invention also describes (1) a

CC corresponding vaccine (V2) against antigens which are not proteins or

CC peptides, as defined above but which have epitopes which show an

CC immunogenic structure; (2) preparing (V1) and (V2); (3) human

CC antidiotopic antibody fragments against the MUC1-conformation epitope

CC having one of 31 approximately 60 residue amino acids sequences, all

CC fully defined in the specification; (4) MUC1-conformation epitope mimics

CC having one of 16 9-17 residue amino acid sequences, all fully in the

CC specification; (5) antidiotopic antibody fragments against the TF

CC antigen having one of 24 approximately 200 residue amino acid sequences,

CC fully defined in the specification; (6) TF carbohydrate epitope mimetics

CC having one of 25 7-13 residue amino acid sequences, all fully defined in

CC the specification; and (7) DNA sequences encoding the fragments and

CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat

CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria

CC and parasites. The vaccines are effective in cases where vaccination has

CC previously not been possible.

XX

SQ Sequence 236 AA;

Query Match 68.2%; Score 907; DB 22; Length 236;

Best Local Similarity 70.0%; Pred. No. 7e-54;

Matches 175; Conservative 28; Mismatches 31; Indels 16; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60

|||||:| | :|| |::|| ||||| | | |||||:||||: || | | |

Db 1 evqlvesggglvqpggslrlscaasgftfssyemnwvrqapgkglewvssgstiyy 60

QY 61 AQKFQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAYHRGSYYMDVWGRG 120

| :|| |::|| : |::: | :|| ||||| : |

Db 61 adsvkgrftisrdnaknsllylqmnsraedtavyycaulpfh-----pwgqg 107

QY 121 TLVTVSSGGGTGGGGGGG-SSELTQDPAVSVALGQTVRITCQGDSLRSYASWYQOK 179

|||||:| | ||||| | |||||:||||: |||||:||||: |||||: |||||

Db 108 tlvtvssgggsgggsggsalseltqdpavsalgtvritcqdslrsyyaswyqqk 167

QY 180 PGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVV 239

|||||:| | ||||| | |||||:||||: |||||:||||: |||||: |||||

Db 168 pgqapvlviygnknrrpsgipdrfsgssgntasltitgaqaedeaddyynsrdsng--tv 225

QY 240 FGGGTKLTVL 249

|||||

Db 226 fgggktltvl 235

```
FT Region 227..237
FT /note= "framework region 4"
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX
PS Disclosure; Fig 7; 89pp; English.
XX
CC The present sequence is that of human single chain antibody (scFv)
CC HIB-3, which is directed against platelet glycoprotein Ib (GPIb).
CC HIB-3 is composed of a heavy chain variable region (see AAY95210)
CC and light chain variable region (see AAY95215) joined via a peptide
CC linker. The HIB series of scFv was isolated from a human synthetic
CC VH and VL scFv library by 3 rounds of phagemid selection against
CC transfected CHO cells expressing the GPIb alpha component of the
CC GPIb/IX/V complex on their surface, followed by a 4th round of
CC selection against washed human platelets, and 2 final rounds in
CC which attempts were made to displace scFv from washed platelets by
CC flooding with murine monoclonal antibody or mimotope peptide (see
CC AAY95229). Whether displayed as surface proteins on a phagemid or
CC secreted as free scFv by Escherichia coli, the HIB scFv clones are
CC capable of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombin
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPIb alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.
XX
SQ Sequence 237 AA;

Query Match 69.7%; Score 926; DB 21; Length 237;
Best Local Similarity 72.0%; Pred. NO. 3.7e-55;
Matches 180; Conservative 25; Mismatches 31; Indels 14; Gaps 3;

OY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFTGYYMYVWROAPGQGLEWMGINPNSGGTNY 60
Db | | | | | : : | | : : | | | | | : | | | | | : | : | | |
OY 1 evqlvesggglvqpqgslrlscaasgftfssyamsvvrqapkgglewvsaisgsgsty 60
Db | | | | | : : | | : : | | | | | : | | | | | : | : | | |
OY 61 ACKFQGRVTMTSDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYYMDVWGRG 120
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
OY 61 adsvkgrftisrdnsksntlylqmslraedtavyyca-----wksllmlwqgg 108
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
OY 121 TLVTVSSGGGGTGGGGSGGG-SSELTQDPAVSVVALGQTVRITCQGDLSRYSYASWYQOK 179
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
OY 109 tlvtvssggggsgggsgsalsseltqdpavsvaigqtvrictqgdsrlrsyasyqqk 168
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
OY 180 PQQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNSRDSGNHV 239
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
OY 169 pggapvlviygnnrpsgipdrfsgsssgntasltitgaqaedeaddyncsrdsghn-v 227
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
OY 240 FGGGTKLTVL 249
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
OY 228 fgggkltvl 237
Db | | | | | : : | | : : | | | | | : | | | | | : | | | | |
```

```
RESULT 14
AAY95198
ID AAY95198 standard; Protein; 238 AA.
XX
AC AAY95198;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human scFv HIB-1.
XX
KW Single chain antibody; scFv; human; HIB-1; glycoprotein Ib alpha;
KW platelet; aggregation; antiaggregant; antithrombotic; thrombus;
KW therapy; diagnostic.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..113 /note= "heavy chain variable region"
FT Region 1..30 /note= "framework region 1"
FT Region 31..34 /note= "complementarity determining region 1"
FT Region 35..49 /note= "framework region 2"
FT Region 50..66 /note= "complementarity determining region 2"
FT Region 67..98 /note= "framework region 3"
FT Region 99..104 /note= "complementarity determining region 3"
FT Region 105..113 /note= "framework region 4"
FT Peptide 114..130 /note= "vector-derived linker"
FT Region 131..238 /note= "light chain variable region"
FT Region 131..152 /note= "framework region 1"
FT Region 153..163 /note= "complementarity determining region 1"
FT Region 164..178 /note= "framework region 2"
FT Region 179..185 /note= "complementarity determining region 2"
FT Region 186..217 /note= "framework region 3"
FT Region 218..226 /note= "complementarity determining region 3"
FT Region 227..238 /note= "framework region 4"
XX WO200026667-A1.
PN 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX
```


C

```
XX US6228599-B1.
PN
XX
PD
XX
XX
PF 26-FEB-1999; 99US-0260527.
PR
XX 24-DEC-1998; 98GB-0028700.
XX (DANI-) DANISCO AS.
XX
XX Knox JP, Willats WGT, Mikkelsen JD;
PI
XX
DR WPI; 2001-342672/36.
DR N-PSDB; AAD06193.
XX
PT New PAM1 and PAM2 antibodies capable of binding de-esterified
PT homogalacturonan, useful for identifying a pectin moiety, for
PT quantifying the amount of pectin in a sample or for extracting pectin
PT from a sample -
XX
PS Claim 1; Fig 4B; 2lpp; English.
XX
CC The invention relates to antibodies specific to pectin, such as PAM1 and
CC PAM2 scFv (single chain variable region). These antibodies are derived
CC from a naive phage display library known as the synthetic scFv Library
CC (#1). PAM1 and PAM2 antibodies are capable of binding to de-esterified
CC and un-substituted homogalacturonan (HG), useful for identifying a pectin
CC motif. PAM antibody is useful for identifying a pectin functional group
CC and in assays to determine if a particular pectin composition has the
CC pectin motif or can be used to prepare a food for human and animal
CC consumption, such as jams, yogurts or gels. The PAM antibodies are
CC further useful for quantifying the amount of pectin in a sample or for
CC extracting pectin from a sample. PAM antibodies are also used to identify
CC de-esterified homogalacturonan blocks in the primary cell walls of
CC plants. The present sequence is PAM1 scFv antibody specific to pectin.
CC Note: This sequence is stated as being the same as that shown as
CC SEQ ID NO: 1 in the sequence listing of the specification, however the
CC sequence has 2 extra residues at the C-terminal end.
XX
SQ Sequence 282 AA;

Query Match 71.6%; Score 951.5; DB 22; Length 282;
Best Local Similarity 73.3%; Pred. No. 8.4e-57;
Matches 184; Conservative 25; Mismatches 29; Indels 13; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFYGMVWVRQAPGQGLEWMGWINPNSGG--T 58
Db 23 evqlvesggglvkpggslrlscaasgftfsnawmswvrqapgkglewgriksktgdgtt 82
QY 59 NYAQKFGQGRVTMTRDTSIGTAYMELSLSSDDTAVYYCARDRIYGSAYHRGSYYMDVWG 118
Db 83 dyaapvkgrftisrddskntlylqmnslktdtavyycar-----kwrkalr----wg 131
QY 119 RGTLTVTSSGGGCTGGGGSGGSELTDQDPAPVSVVALGQTVRITCGDLSRYYASWYQQ 178
Db 132 qgtltvtsrsgggsgggsgsseltqdpavsvvalgqtvritcgdsrlrsyyaswyqq 191
QY 179 KPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHV 238
Db 192 kpgqapvlviygnknrpsgipdrfsgsssgntasltitgaqaedeaddyccnsrdssgnhv 251
QY 239 VEGGKTKLTVL 249
Db 252 vfgggtklcvtl 262

RESULT 11
AAW49693
ID AAW49693 standard; Protein; 254 AA.
XX
AC AAW49693;
```

```
XX 10-NOV-1998 (first entry)
DT
XX
DE Human ScFv4 against alpha-1,3-galactosyl transferase.
XX
KW Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
KW sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
KW graft tissue rejection; organ transplantation; xenotransplant; human;
KW single chain antibody.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN FR2751346-A1.
XX
PD 23-JAN-1998.
XX
PF 19-JUL-1996; 96FR-0009077.
XX
PR 19-JUL-1996; 96FR-0009077.
XX
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Pourcel C, Souillou JP, Vanhove B;
PI
XX WPI; 1998-112876/11.
DR N-PSDB; AAV49460.
DR
XX
PT Transgenic non-human donors of organs for human recipients -
PT containing DNA encoding antibodies that inhibit graft rejection
PT
XX
PS Claim 6; Page 53-54; 7lpp; French.
XX
CC This sequence represents a single chain antibody (ScFv4) constructed from
CC the sequence encoding a human antibody raised against the porcine enzyme
CC alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses
CC the attachment of a galactose sugar molecule on the N-acetyllactosamine
CC moiety found on surface glycoproteins and glycolipids. These sugar
CC molecules are partly responsible for raising anti-graft antibodies, which
CC lead to graft tissue rejection. The invention relates to a method of
CC inhibiting the graft rejection mechanism by introducing the sequence
CC encoding an antibody targeted to alpha-1,3-GT into the cells of animal,
CC especially a pig, from whom organs may be used for xenotransplants.
CC Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking
CC the galactose on the glycoproteins and glycolipids, thus preventing
CC induction of the rejection response.
XX
SQ Sequence 254 AA;

Query Match 71.3%; Score 947.5; DB 19; Length 254;
Best Local Similarity 72.3%; Pred. No. 1.4e-56;
Matches 180; Conservative 27; Mismatches 29; Indels 13; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFYGMVWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 12 qvqlvqsgggglvqpqgslrlscaasgftfssysmnwvrqapgkglewsvyisssstiy 71
QY 61 AQKFQGRVTMTRDTSIGTAYMELSLSSDDTAVYYCARDRIYGSAYHRGSYYMDVWGRG 120
Db 72 adsvkgrftisrdnaknsllylqmnsldtdtavyyctr-----awrtd-wggg 118
QY 121 TLTVTVSSGGGCTGGGGSGGSELTDQDPAPVSVVALGQTVRITCGDLSRYYASWYQQKP 180
Db 119 tltvtsrsgggsgggsgggsseltqdpavsvvalgqtvritcgdsrlrsyyaswyqqkp 178
QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240
Db 179 gqapvlviygnknrpsgipdrfsgsssgntasltitgaqaedeaddyccnsrdssgnhv 238
QY 241 GGGTKLTVL 249
Db 239 ggggtklcvtl 247
```


QY 74 TSIGTAYMELSLSSDDTAVYVCARDRYYGSSAYHRGSYMDVWGRGTLVTVSSGGGTG 133
II IIIII I I:IIIIII I
Db 61 tsastaymelsslrstdtavycarsgy-----wgqgtlvtvsrgggsg 106
IIIIII I I:IIIIII I
QY 134 GCGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYASWYQKPGCAPVLVIYCKNN 193
IIIIII I I:IIIIII I
Db 107 gggsgggsseltqdpavsalgqtvritcqgdsrlrsyyaswyqkpgqapvlviygnn 166
IIIIII I I:IIIIII I
QY 194 RPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFFGGTKLTVL 249
IIIIII I I:IIIIII I
Db 167 rpsgipdrfsgsssgntasltitgaqadeadyycnsrdssgnhvvfgggtklvtl 222
IIIIII I I:IIIIII I
RESULT 7
AAB67619
ID AAB67619 standard; Protein; 245 AA.
XX
AC AAB67619;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_3.
XX
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
XX
OS Homo sapiens.
XX
PN WO200114558-A1.
XX
PD 01-MAR-2001.
XX
PF 28-AUG-2000; 2000WO-EP08388.
XX
PR 26-AUG-1999; 99EP-0116691.
XX
XX (MORP-) MORPHOSYS AG.
PA
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;
XX WPI; 2001-218451/22.
DR
XX
PT Novel isolated human immunoglobulin or functional immunoglobulin
PT fragment specific for human leukocyte antigen Cw6, useful for treatment
PT of humans and for human leukocyte antigen phenotyping -
XX
PS Claim 3; Fig 1; 23pp; English.
XX
CC AAB67617-23 represent single chain antibody (scFv) fragments which
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
CC derived from a synthetic human combinatorial antibody library based on
CC molecular consensus frameworks and CDRs randomised with trinucleotides.
CC The specification describes a human immunoglobulin fragments specific
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
CC studies of natural killer cell silencing as well as miscarriages.
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
CC fragments are useful for the preparation of a pharmaceutical for the
CC treatment of humans. They are also useful for HLA phenotyping.
XX
SQ Sequence 245 AA;

Query Match 76.1%; Score 1011.5; DB 22; Length 245;
Best Local Similarity 77.0%; Pred. No. 6.6e-61;
Matches 197; Conservative 19; Mismatches 21; Indels 19; Gaps 4;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
:IIIIII I I:IIIIII I
Db 1 qvqlvqsgaevkpgasvkvsckasgytftsyyhmhwrqapggglewmgwinpnsqgtny 60
IIIIII I I:IIIIII I
QY 61 AOKFQGRVTMTSDTSIGTAYMELSLSSDDTAVYYCARDRYYGSSAYHRGSY-YMDVWGR 119
IIIIII I I:IIIIII I

Db 61 aqkfqgrvtmtrdtsistaymelsslrstdtavyyca-----rgsfdfmdnwqg 109
IIIIII I I:IIIIII I
QY 120 GTLVTVSSGGGTGGGGSGGGSS-----ELTQDPAVSVALGQTVRITCQGDSLRSYA 173
IIIIII I I:IIIIII I
Db 110 gtlvtvssagggsgggsgggsgggsgdieltqppsvsvapqqtariscsgdalqdkya 169
IIIIII I I:IIIIII I
QY 174 SWYQOKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDS 233
IIIIII I I:IIIIII I
Db 170 swyqkpgqapvlviyddsdprsgiperfsgsngntatltisgtqaedeaddyocsydd 229
IIIIII I I:IIIIII I
QY 234 SONHVFFGGTKLTVL 249
: :IIIIII I
Db 230 t-dlivfgggtklvtl 244
IIIIII I I:IIIIII I
RESULT 8
AAW83322
ID AAW83322 standard; Protein; 309 AA.
XX
AC AAW83322;
XX
DT 16-MAR-1999 (first entry)
XX
DE Single chain Apo-2 antibody 16E2.
XX
KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW TNF cytokine.
XX
OS Homo sapiens.
XX
PN WO9851793-A1.
XX
PD 19-NOV-1998.
XX
PF 14-MAY-1998; 98WO-US09704.
XX
PR 09-FEB-1998; 98US-0020746.
PR 15-MAY-1997; 97US-0857216.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI; 1999-045228/04.
DR N-PSDB; AAV72532.
DR
XX
PT Human Apo-2 polypeptide inducing apoptosis - useful to treat
PT conditions linked with decreased apoptosis e.g. cancer, and produce
PT antibodies to increase or decrease apoptosis
PS Example 14; Fig 16; 134pp; English.
XX
CC The present invention describes human Apo-2. Apo-2 can be used
CC therapeutically to induce apoptosis in mammalian cells, and so is useful
CC to treat conditions associated with decreased apoptosis e.g. cancer.
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
CC can be used to identify agents activating Apo-2, useful to treat
CC mammalian cancer cells, and to produce Apo-2 chimeras useful
CC therapeutically (e.g. those containing immunoglobulin sequences can be
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
CC tag polypeptide allow Apo-2 detection and purification using anti-tag
CC antibodies). It can be used to produce antibodies which can be combined
CC with a (particularly pharmaceutically acceptable) carrier in compositions
CC or used to produce dimeric molecules (especially homodimeric molecules
CC comprising first and second Apo-2 antibodies). Agonistic (especially
CC single-chain) antibodies can be administered to induce apoptosis in
CC mammalian cancer cells, and antagonistic antibodies used to block
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
CC antibodies may also be used diagnostically e.g. to detect Apo-2
CC expression in cells/tissues and in Apo-2 purification. The present

KW sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
KW graft tissue rejection; organ transplantation; xenotransplant; human;
XX single chain antibody.
OS Synthetic.
OS Homo sapiens.
XX FR2751346-A1.
PN
XX
PD 23-JAN-1998.
XX
PF 19-JUL-1996; 96FR-0009077.
XX
PR 19-JUL-1996; 96FR-0009077.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Pourcel C, Soullilou JP, Vanhove B;
XX
XX WPI; 1998-112876/11.
DR N-PSDB; AAV49458.
XX
PT Transgenic non-human donors of organs for human recipients -
PT containing DNA encoding antibodies that inhibit graft rejection
XX
PS Claim 6; Page 48-49; 71pp; French.
XX
CC This sequence represents a single chain antibody (ScFv2) constructed from
CC the sequence encoding a human antibody raised against the porcine enzyme
CC alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses
CC the attachment of a galactose sugar molecule on the N-acetyllactosamine
CC moiety found on surface glycoproteins and glycolipids. These sugar
CC molecules are partly responsible for raising anti-graft antibodies, which
CC lead to graft tissue rejection. The invention relates to a method of
CC inhibiting the graft rejection mechanism by introducing the sequence
CC encoding an antibody targeted to alpha-1,3-GT into the cells of animal,
CC especially a pig, from whom organs may be used for xenotransplants.
CC Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking
CC the galactose on the glycoproteins and glycolipids, thus preventing
CC induction of the rejection response.
XX
SQ Sequence 237 AA;

Query Match 80.8%; Score 1073.5; DB 19; Length 237;
Best Local Similarity 83.5%; Pred. No. 4.2e-65;
Matches 208; Conservative 8; Mismatches 20; Indels 13; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db :|||||
1 qvqlvsgaevkpgasvkvsckvsgytltelsmhvvrqapgkglewmggfdpedgetiy 60

QY 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAYHRGSYYMDVWGRG 120
Db :|||||
61 aqkfggrvmtedtstdtaymelsslrsestavyycarpe-----idqwgqg 107

QY 121 TLVTYSSGGGTGGGGSGGSELTDQPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180
Db :|||||
108 tlvtvsrgggsgggsgggsseltqdpavsvvalgqtvritcqqgslrsyyaswyqqkp 167

QY 181 GQAPVLVIYGNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGSHVVF 240
Db :|||||
168 gqapvlviygnnrpsgipdrfsgsssgntasltitgaqacdeadyycnsrdssgshvvf 227

QY 241 GCGTKLTVL 249
Db :|||||
228 gggtkltvl 236

RESULT 4
AAW49692
ID AAW49692 standard; Protein; 239 AA.
XX

AC AAW49692;
XX
DT 10-NOV-1998 (first entry)
XX
DE Human ScFv3 against alpha-1,3-galactosyl transferase.
XX
KW Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
KW sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
KW graft tissue rejection; organ transplantation; xenotransplant; human;
KW single chain antibody.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN FR2751346-A1.
XX
PD 23-JAN-1998.
XX
PF 19-JUL-1996; 96FR-0009077.
XX
PR 19-JUL-1996; 96FR-0009077.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Pourcel C, Soullilou JP, Vanhove B;
XX
XX WPI; 1998-112876/11.
DR N-PSDB; AAV49459.
XX
PT Transgenic non-human donors of organs for human recipients -
PT containing DNA encoding antibodies that inhibit graft rejection
XX
PS Claim 6; Page 51-52; 71pp; French.
XX
CC This sequence represents a single chain antibody (ScFv3) constructed from
CC the sequence encoding a human antibody raised against the porcine enzyme
CC alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses
CC the attachment of a galactose sugar molecule on the N-acetyllactosamine
CC moiety found on surface glycoproteins and glycolipids. These sugar
CC molecules are partly responsible for raising anti-graft antibodies, which
CC lead to graft tissue rejection. The invention relates to a method of
CC inhibiting the graft rejection mechanism by introducing the sequence
CC encoding an antibody targeted to alpha-1,3-GT into the cells of animal,
CC especially a pig, from whom organs may be used for xenotransplants.
CC Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking
CC the galactose on the glycoproteins and glycolipids, thus preventing
CC induction of the rejection response.
XX
SQ Sequence 239 AA;

Query Match 80.1%; Score 1064.5; DB 19; Length 239;
Best Local Similarity 81.5%; Pred. No. 1.7e-64;
Matches 203; Conservative 12; Mismatches 23; Indels 11; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db :|||||
1 qvqlvsgaevkpgasvkvsckasgytftsamnwvrqapggglewmgwintntgnty 60

QY 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAYHRGSYYMDVWGRG 120
Db :|||||
61 aqkfggrvmtedtstdtaymelsslrsestavyycarpe-----rsndpadqwgqg 109

QY 121 TLVTYSSGGGTGGGGSGGSELTDQPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180
Db :|||||
110 tlvtvsrgggsgggsgggsseltqdpavsvvalgqtvritcqqgslrsyyaswyqqkp 169

QY 181 GQAPVLVIYGNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGSHVVF 240
Db :|||||
170 gqapvlviygnnrpsgipdrfsgsssgntasltitgaqacdeadyycnsrdssgshvvf 229

QY 241 GCGTKLTVL 249
Db :|||||

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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:24:03 ; Search time 101.13 Seconds
(without alignments)
273.483 Million cell updates/sec

Title: US-08-779-457-48
Perfect score: 1329
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*

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17: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*

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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1329	100.0	249	AAW24061	Human WSX receptor
2	1104	83.1	236	AAW49690	Human SCFv1 against
3	1073.5	80.8	237	AAW49691	Human SCFv2 against
4	1064.5	80.1	239	AAW49692	Human SCFv3 against
5	1064	80.1	242	AAV15127	Anti-murine CTLA-4
6	1051	79.1	229	AAW49694	Human SCFv5 against
7	1011.5	76.1	245	AAW67619	Human leukocyte an
8	997	75.0	309	AAW83322	Single chain Apo-2
9	963.5	72.5	312	AAW83323	Single chain Apo-2
10	951.5	71.6	282	AAE02185	PAM1 single chain
11	947.5	71.3	254	AAW49693	Human SCFv4 against

12	936	70.4	240	22	AAW46052	Human TF anti-idio
13	926	69.7	237	21	AAW95219	Anti-platelet glyc
14	924	69.5	238	21	AAW95198	Anti-platelet glyc
15	907	68.2	236	22	AAW46055	Human TF anti-idio
16	906.5	68.2	245	22	AAW67618	Human leukocyte an
17	904.5	68.1	245	22	AAW67617	Human leukocyte an
18	904	68.0	242	22	AAW46053	Human TF anti-idio
19	894.5	67.3	239	22	AAW46054	Human TF anti-idio
20	884.5	66.6	280	22	AAE02186	PAM2 single chain
21	865.5	65.1	245	22	AAW67621	Human leukocyte an
22	865.5	65.1	245	22	AAW67622	Human leukocyte an
23	865.5	65.1	245	22	AAW67623	Human leukocyte an
24	831.5	62.6	249	21	AAW36083	Recombinant human
25	826.5	62.2	250	18	AAW24062	Human WSX receptor
26	809.5	60.9	245	22	AAW67620	Human leukocyte an
27	792	59.6	304	22	AAW63634	Amino acid sequenc
28	792	59.6	304	22	AAW63639	Amino acid sequenc
29	773.5	58.2	258	18	AAW08487	C6 human sfv antib
30	767.5	57.8	310	20	AAW83324	Single chain Apo-2
31	763.5	57.4	256	13	AAW22583	ScFvB18 construct
32	763.5	57.4	428	18	AAW24027	Single chain antig
33	763.5	57.4	443	18	AAW24025	Single chain antig
34	760.5	57.2	402	15	AAW56485	ScFV PRAS110 and p
35	758.5	57.1	269	15	AAW54756	PRAS111 between H1
36	757.5	57.0	256	13	AAW22584	ScFvB18 construct
37	757.5	57.0	435	15	AAW56483	ScFV PRAS108 and p
38	756.5	56.9	241	20	AAW21882	Amino acid sequenc
39	755.5	56.8	269	15	AAW56482	ScFV PRAS107 and p
40	754.5	56.8	256	13	AAW22568	ScFvB18 construct.
41	754	56.7	250	21	AAW44346	3B3 antibody. Hom
42	750.5	56.5	256	13	AAW22582	ScFvB18 construct
43	749.5	56.4	415	15	AAW56484	ScFV PRAS109 and p
44	748.5	56.3	256	13	AAW22585	ScFvB18 construct
45	748.5	56.3	256	13	AAW22587	ScFvB18 construct

ALIGNMENTS

RESULT 1

AAW24061

ID AAW24061 standard; Protein; 249 AA.

XX

AC AAW24061;

XX

DT 17-MAR-1998 (first entry)

XX

DE Human WSX receptor agonist antibody clone #3.

XX

KW Human; WSX receptor; clone #3; identification; purification;

KW ligand; activator; antibody; agonist; proliferation; obesity;

KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;

KW Type II diabetes; polycystic ovarian disease;

KW cardiovascular disease; osteoarthritis; dermatological disorder;

KW hypertension; insulin resistance; hypercholesterolaemia;

KW hypertriglyceridaemia; cancer; cholelithiasis.

XX

OS Homo sapiens.

XX

PN W09725425-A1.

XX

PD 17-JUL-1997.

XX

PF 07-JAN-1997; 97WO-US00325.

XX

PR 20-JUN-1996; 96US-0667197.

PR 08-JAN-1996; 96US-0585005.

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PA (GETH) GENENTECH INC.

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PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

PI Rodrigues ML;

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RESULT 9

PH0961
Ig heavy chain V region (G6+ T-L33) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0961
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-119 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-107/Region: complementarity-determining 3

Query Match 39.8%; Score 517; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 2.2e-27;
Matches 102; Conservative 7; Mismatches 10; Indels 6; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANY 60
QY 61 AQKFGQGRVTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGQGRVTITADESTAYMELSSLRSEDTAVYYCARGYYY- - - - - YGMDVWGQGT 114
QY 121 VTVSS 125
:|||||
Db 115 VTVSS 119
:|||||

RESULT 10

S44105
Ig lambda chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44105
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44105
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <HAW>
A;Cross-references: EMBL:Z31388; NID:g472959; PIDN:CAA83263.1; PID:g940517
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 513.5; DB 2; Length 112;
Best Local Similarity 91.0%; Pred. No. 3.5e-27;
Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 141 QSVLTQPASVSGSPGQSITISCTGTSSDVGGYVSNVYQHPGKAPKLMIEGSKRPSGV 200
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QSALTQPASVSGSPGQSITISCTGTSSDVGGYVSNVYQHPGKAPKLMIDVSNRPSGV 60
QY 201 SNRFGSGKSGSTASLTISGLQAEDEADYYCSTYTRSTR-VFGGGTKLTVL 250
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SNRFGSGKSGNTASLTISGLQAEDEADYYCSTYTRSTRVFGTGKTVL 111

RESULT 11

PH0957
Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0957
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0957
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-125 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-113/Region: complementarity-determining 3

Query Match 39.5%; Score 513; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 4.3e-27;
Matches 100; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAINWVRQAPGQGLEWMGGIPIFGTANY 60
QY 61 AQKFGQGRVTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGQGRVTITADESTAYMELSSLRSEDTAVYYCARDGCGSGGSCYFWGWFDPWGQGT 120
QY 121 VTVSS 125
:|||||
Db 121 VTVSS 125
:|||||

RESULT 12

PH0955
Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0955
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0955
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-127 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-115/Region: complementarity-determining 3

Query Match 39.2%; Score 509; DB 2; Length 127;
Best Local Similarity 80.3%; Pred. No. 7.9e-27;
Matches 102; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-124/Region: complementarity-determining 3

Query Match 40.5%; Score 526.5; DB 2; Length 136;
Best Local Similarity 76.5%; Pred. No. 6.1e-28;
Matches 104; Conservative 10; Mismatches 11; Indels 11; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGFTFSSYKMNWVRQAPGQGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRG----- 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGTRVSVSTLYDSSGYDFSGY 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 111 -GMDVWGQGTITVTVSS 125
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 YGMDVWGQGTITVTVSS 136
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
C33548
Ig heavy chain V-1 region (783) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: C33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression
A:Reference number: A33548; MUID:89345575
A:Accession: C33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-133 <KIP>
A:Experimental source: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 40.3%; Score 524; DB 2; Length 133;
Best Local Similarity 77.4%; Pred. No. 8.7e-28;
Matches 103; Conservative 11; Mismatches 11; Indels 8; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGFTFSSYKMNWVRQAPGQGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRG-----LRGGM 112
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTKILGPYSSGWPNSDYVYGM 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 113 DVWGQGTITVTVSS 125
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 DVWGQGTITVTVSS 133
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
PH0958
Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0958
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0958

A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-122 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-110/Region: complementarity-determining 3

Query Match 40.0%; Score 519.5; DB 2; Length 122;
Best Local Similarity 82.4%; Pred. No. 1.6e-27;
Matches 103; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGFTFSSYKMNWVRQAPGQGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGMDVWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR---VPNPLFFAVGMDVWGQGT 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 VTVSS 125
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 118 VTVSS 122
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0954
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0954
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-132 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-120/Region: complementarity-determining 3

Query Match 39.9%; Score 518.5; DB 2; Length 132;
Best Local Similarity 75.9%; Pred. No. 2e-27;
Matches 104; Conservative 8; Mismatches 8; Indels 17; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGFTFSSYKMNWVRQAPGQGLEWMGGIPIFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRG----- 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR-----PHASIDDFWSGYYPNY 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 111 -GMDVWGQGTITVTVSS 125
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 116 YGMDVWGQGTITVTVSS 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:25:01 ; Search time 54.95 Seconds
(without alignments)
437.167 Million cell upd

Title: US-08-779-457-49
 Perfect score: 1300
 Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SSYTRSTRVFGGCKLTVL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:	283138
----------------------------------------------------	--------

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :      PIR_71:**
1:  pir1:**
2:  pir2:**
3:  pir3:**
4:  pir4:**
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648.5	49.9	268	2 A56446	Ig heavy chain V r
2	628	48.3	249	2 S41374	single chain Fv an
3	591	45.5	233	2 JC5322	p53 specific singl
4	537.5	41.3	627	2 S14683	Ig mu chain precur
5	526.5	40.5	136	2 PH0960	Ig heavy chain v r
6	524	40.3	133	2 C33548	Ig heavy chain v-1
7	519.5	40.0	122	2 PH0958	Ig heavy chain v r
8	518.5	39.9	132	2 PH0954	Ig heavy chain v r
9	517	39.8	119	2 PH0961	Ig heavy chain v r
10	513.5	39.5	112	2 S44105	Ig lambda chain v-
11	513	39.5	125	2 PH0957	Ig heavy chain v r
12	509	39.2	127	2 PH0955	Ig heavy chain v r
13	506	38.9	111	1 L2HUN1	Ig lambda chain v-
14	504.5	38.8	126	2 B33548	Ig heavy chain v-1
15	503.5	38.7	120	2 PH0962	Ig heavy chain v r
16	501.5	38.6	112	2 S44123	Ig lambda chain v-
17	501.5	38.6	132	2 S46394	Ig heavy chain v r
18	500	38.5	129	2 A33548	Ig heavy chain v-1
19	498.5	38.3	112	2 S31515	Ig lambda chain v
20	497	38.2	111	2 S36281	Ig lambda chain v
21	496.5	38.2	116	2 PH0959	Ig heavy chain v r
22	496.5	38.2	128	2 PH0952	Ig heavy chain v r
23	494.5	38.0	112	1 L2HUNG	Ig lambda chain v-
24	494.5	38.0	112	2 S46395	Ig lambda chain v
25	493	37.9	111	2 S46396	Ig lambda chain v
26	492	37.8	135	2 PH0953	Ig heavy chain v r
27	487	37.5	235	2 S25758	Ig lambda chain -
28	483	37.2	111	2 S36256	Ig lambda chain v
29	481.5	37.0	135	2 B32274	Ig heavy chain pre

ALIGNMENTS

RESULT 1

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
 C:Accession: A56446
 R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. BIOL. CHEM. 270, 7829-7835, 1995
 A>Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the native protein
 A:Reference number: A56446; MUID:95229583

A: Accession: A56446

A; Status: preliminary

A; Molecule type: mRNA

A; ResIdues: 1-268 <TAN>

A; Cross-references: GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 49.9%; Score 648.5; DB 2; Length 268;
Best Local Similarity 53.6%; pred. No. 1.3e-35;
Matches 134: Conservative 33; Mismatches 70; Indels 13

Qy	1	EVQLVQSGAEVKKPGESLKISCSQSGSFTSSYKMNWVRQAPKGLEWMGGIIPIFGTANY	60
Dd	3	QVKLQESGAELVKPGASVKLSCTSGFNKIDTYMHWVKRQPEQGLEWIGRIAPANGITKY	62
Qy	61	AQKFQGRVITITADESTSTAYMELSSLRSEDTAIVYCARDRVVVPATSLRGGMDVWGQTT	120
Dd	63	DPKFQGRATIAADTSSNTAYLQLSSLTSEDTAIVYCA-----SYLTRYENYWGQTT	115
Qy	121	VTVSSGGGSGGGSGGGGSQSVLTQ-PASVSGSPGQSITISCTGTSSDVGGINYVSWYQ	179
Dd	116	VTVSSGGGSGCGDSDGGGSDIELTQSPAIMASLGEKVTMSCRASSS-----VNFIYVYQ	171
Qy	180	QHPGKAPKLMIYEGSKRPPSGVSNRFGSKSGSTASLTISGLQAEDEADYICSSYTRRSTR	239
Dd	172	QKSDASPKLWVYVYTHLPPGVPAFSGSGSGNSYSLTSSMEGEDAATYYCQQQFTS-SPF	230

RESULT 2

S41374

single chain Fv antibody - mouse

C; Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C;Accession: S41374

R; Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A;Description: Construction and functional characterization of a single chain Fv anti-

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

Query Match          54.4%; Score 723.5; DB 4; Length 673;
Best Local Similarity 55.1%; Pred. No. 4.4e-52;
Matches 141; Conservative 44; Mismatches 54; Indels 17; Gaps 5;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 20 QVQLQQPGAELVKPGASVQLSCKASGYTFTGYWIHWVKQRPCQGLEWIGEVNPSTGRSDY 79

QY 61 AQKFGGRVTMTTRDTSIGTAYMELSRLLSSDDTAVYYCARDRYVYSSAYHRGSYYMDVWGRG 120
Db 80 NEKFNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARERAYGYDD-----AMDIWGGG 133

QY 121 TLVTYSSGGGGTGGGGGGSS-ELTQDP-AVSVALGQTVRITCQGDS-----LRSYY 172
Db 134 TTVTVSSGGGGGGGGGGGGSDIELSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNY 193

QY 173 ASNYQOKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRD 232
Db 194 LAWYQQRPGQSPKLLIYWASTRTSGVPDRFTGSGSGTDFTLTISVQAEDLAIYYCK--- 250

QY 233 SSGNHVVEGGGTKLTV 248
Db 251 QSYTLRTFEGGKLEI 266
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Search completed: August 15, 2002, 16:22:14
Job time: 424 sec


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; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-20

Query Match 54.7%; Score 727.5; DB 2; Length 244;
Best Local Similarity 58.4%; Pred. No. 6.2e-53;
Matches 146; Conservative 31; Mismatches 64; Indels 9; Gaps 4;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYVVRQAPQGQGLEWMGWINPNSGGTNY 60
Db 1 EVQLQSGAELVKPGASVKLSCKASGYTFTSHWHVYKQKQAGQGLEWGFNPSNCRNTY 60

QY 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAYHRGSYYNDVWGRG 120
Db 61 NEKFKSKATLTVDKSSSTAYMQLSSTSEDSAVYYCA-----SRDYDYGDFYWGQG 114

QY 121 TLVTSSGGGTGGGGGGSS-ELTQDPV-SVALGQTVRITCOGDSLRSYASWYQQ 178
Db 115 TTVTVSSGGGTGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSVS-YMYWYQQ 173

QY 179 KPGQAPVLIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHV 238
Db 174 KPGSSPRLLIYDTNLASGVPVRFSGSGSGTSYSLTISRMEAEADAATYYCQWSSYPPMY 233

QY 239 VEGGGTKLTV 248
Db 234 TFGGGTKLEI 243

RESULT 14
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423.439
; FILING DATE: 09-NO. 6339070-1999
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-20
```

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match 54.4%; Score 723.5; DB 4; Length 288;
Best Local Similarity 55.1%; Pred. No. 1.6e-52;
Matches 141; Conservative 44; Mismatches 54; Indels 17; Gaps 5;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYVVRQAPQGQGLEWMGWINPNSGGTNY 60
Db 23 QVQLQQPGAEVKKPGASVQLSCKASGYTFTGYWIHWVKQKQPGQGLEWIEVNPSTGRSDY 82

QY 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAYHRGSYYMDVWGRG 120
Db 83 NEKEFNKATLTVDKSSSTAYMQLSSTSEDSAVYYCAREAYGYDD-----AMDYWGQG 136

QY 121 TLVTSSGGGTGGGGGGSS-ELTQDP-AVSVALGQTVRITCOGDS-----LRSYV 172
Db 137 TTVTVSSGGGTGGGGGGSDIELSQSPSSLAWSAGEKVTMSCKSSQSLLSNRTRKNY 196

QY 173 ASWYQQKPGQAPVLIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRD 232
Db 197 LAWYQQRPGQSPKLLIYNASTRTSGVPDRFTGSGSGTDFLTITSSVQAEDLAIYVCK--- 253

QY 233 SSGNHVVEGGGKLTV 248
Db 254 QSYTLRTFGGGTKLEI 269

RESULT 15
US-09-423-439-32
; Sequence 32, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423.439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32
```

```

US-08-491-988-5
; Sequence 5, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMEMNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,988
; FILING DATE: 18-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-988-5

```

```

Query Match      57.1%; Score 758.5; DB 2; Length 435;
Best Local Similarity 60.1%; Pred. NO. 3.4e-55;
Matches 152; Conservative 35; Mismatches 53; Indels 13; Gaps 4;

QY   1 EVQLVQSGAEVKPGASVKVSCKASGYFTFGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
      :||| | ||| :|||||:||||| ||| |:|:| | |||:| |:||||| |
Db   23 QVQLQQPGAELKPGASVKLSCKASGYFTSYMMHWVKORPGRGLEWIGRIDPNSSGGTKY 82
      :||| | ||| :|||||:||||| ||| |:|:| | |||:| |:||||| |
QY   61 AQKFQGRVTMTTRDTSTGTAYMELSLRLSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRC 120
      :||| : | :| | |||:| | |:|:| ||||| ||||| | | ||| :|
Db   83 NEKFKSATLTVDKPSSTAYMQLSLTSDES AVYYCARDYDYGSS-----YFDYWGGQ 135
      :||| : | :| | |||:| | |:|:| ||||| ||||| | | ||| :|
QY   121 TLTVTVSSGGGGTGGCGSGGGGS -SELTQDPAVSVALGQTVRITCQ---GDSLRSYYASWY 176
      | ||||| |||:||||| ||| : ||| :| :| ||| :||| : | ||| :|
Db   136 TTIVTVSSGGGGSGGGCGGGGQA VVTQESALTTSPEGEIVTLTCRSSTGA VTTSYANWV 195
      | ||||| |||:||||| ||| : ||| :| :| ||| :||| : | ||| :|
QY   177 QQKPGQAPLVIIYGNRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNRRDSSGN 236
      | :|| : | ||| | :| |||| |:|:||||| ||||| ||| :| |
Db   196 QEKPDHLFTGLIGGTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYS--N 253
      | :|| : | ||| | :| |||| |:|:||||| ||||| ||| :| |
QY   237 HWVFGGGTKLTVL 249
      | ||||| |||||
Db   254 HWVFGGGTKLTVL 266

```

RESULT 12
US-08-918-148-74
; Sequence 74, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.

```
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 74  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-74
```

Query Match 55.4%; Score 736.5; DB 4; Length 249;
Best Local Similarity 57.3%; Pred. No. 1.2e-53;
Matches 145; Conservative 40; Mismatches 55; Indels 13; Gaps 5;

QY	1	EVQLVQSGAEVKKPGASVKVSCKASGYFTFGYYMYWVRQAPGCGLEWMGWINPNSGGTNY	60
DQ	3	QVQLQESGGEMKKPGESLKISCKGYGSFATSWIGWVRQMPGRGLEWMAIMYPGNSDTRH	62
QY	61	AQKFQGRVTMTTRDTISCTAYMELSRSLSSDDTAIVYYCARDRYYGSSAYHRGSYYMDVMGRG	120
DQ	63	NPSFEDQVMTSADTSINTAYLQWSSLKASDTAMYICARAGVAGGA-----FDLWGKG	114
QY	121	TLTVTVSSGGGTGGGGGGGGG--SELTQDPAVSVVALGQTVRITCQGDS--LRSY-YASWY	176
DQ	115	TMTVTVSSGGGGGGGGGGGQSQSVLTQPASVSGSPGQSITISCTGTSSGVGGYNYVSWY	174
QY	177	QQKPQGPAPLVIIYGNRRPSGIPDRFSGSSSGNTASLTITGAQAQEADEADYYCNRSRDSGN	236
DQ	175	QQHPGKAPKLLIYGNNSRPSGVPRFRFSASKSGNTASLTISGLQAQEADEADYFCSTYAPPG-	233
QY	237	HVFVGSGTKLTVL	249
DQ	234	IIMFGGGTKLTVL	246

RESULT 13
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCES
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCES
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:


```
QY 61 AOKFQGRVTMTDTSIGTAYMELSLRLSSDDTAVYYCARDRIYSSAYHRRGSYYMDVWGRG 120
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 100 ADSVKGRVTISRDNKNSLYLQMNLSLRAEDTAVYYCAKILGAG-----RG-WYFDLWKGK 153
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 121 TLVTVSSGGGTGGGGSSSELTDQPAVSVALGQTVRITCQGDSLRSLRYYASWYQOKP 180
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 154 TTVTVSSGGGTGGGGSSSELTDQPAVSVALGQTVRITCQGDSLRSLRYYASWYQOKP 213
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 181 GQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVF 240
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 214 GQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHVF 273
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 241 GGGTKLTVL 249
      :|||||:|
Db 274 GGGTKLTVL 282
      :|||||:|

RESULT 2
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camillia W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10

Query Match 72.5%; Score 963.5; DB 4; Length 312;
Best Local Similarity 73.6%; Pred. No. 2.7e-72;
Matches 184; Conservative 26; Mismatches 33; Indels 7; Gaps 2;

QY 2 VOLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNYA 61
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 41 VOLVESGGGLVQPGGSLRLSCAASGFTFSYWMWVRQAPGKGLEWVANIKQDGSEKYYV 100
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 62 QKFQGRVTMTDTSIGTAYMELSLRLSSDDTAVYYCARD--RYYGSSAYHRRGSYYMDVWGR 119
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 101 DSVKGRFTISRDNKNSLYLQMNLSLRAEDTAVYYCARDLLKVKGSS-----SGWFDPWGR 155
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 120 GTLVTVSSGGGTGGGGSSSELTDQPAVSVALGQTVRITCQGDSLRSLRYYASWYQOK 179
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
```

```
Db 156 GTTIVTSSGGGTGGGGSSSELTDQPAVSVALGQTVRITCQGDSLRSLRYYASWYQOK 215
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 180 PGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHV 239
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 216 PGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHV 275
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 240 FGGGTKLTVL 249
      :|||||:|
Db 276 FGGGTKLTVL 285
      :|||||:|

RESULT 3
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scFv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

Query Match 71.6%; Score 951.5; DB 4; Length 280;
Best Local Similarity 73.3%; Pred. No. 2.4e-71;
Matches 184; Conservative 25; Mismatches 29; Indels 13; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGG--T 58
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 23 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWGRISKTGGTT 82
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 59 NYAQKFQGRVTMTDTSIGTAYMELSLRLSSDDTAVYYCARDRIYSSAYHRRGSYYMDVWG 118
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 83 DYAAPVKGRFTISRDDSKNTLYLQMNLSLKTEDTAVYYCAR-----KWRKALR---WG 131
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 119 RGTLVTVSSGGGTGGGGSSSELTDQPAVSVALGQTVRITCQGDSLRSLRYYASWYQQ 178
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 132 QGTLVTVSRGGCGSGGGSSSELTDQPAVSVALGQTVRITCQGDSLRSLRYYASWYQQ 191
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 179 KPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHV 238
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
Db 192 KPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGHNHV 251
      :|||||:| : :|:|:| :|:|:|:|:|:| :|:|:|:|:|:| :|:|:|:|:|:|
QY 239 VFGGGTKLTVL 249
      :|||||:|
Db 252 VFGGGTKLTVL 262
      :|||||:|

RESULT 4
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:27:05 ; Search time 111.01 Seconds
(without alignments)
518.318 Million cell updates/sec

Title: US-08-779-457-48
Perfect score: 1329
Sequence: 1 EVQLVQSGAEVKKPGASVKV.....SRDSSGNHVVFGGTKLTVL 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 698052 seqs, 231078099 residues

Total number of hits satisfying chosen parameters: 698052

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1101.5	82.9	262	5	US-09-791-537-39412
2	1098.5	82.7	262	5	US-09-791-537-121575
3	1076	81.0	250	1	PCT-US02-16106-20
4	1076	81.0	250	6	US-10-151-882-20
5	967.5	72.8	262	5	US-09-791-537-1444
6	928.5	69.9	253	5	US-09-791-537-118537
7	906	68.2	290	5	US-09-949-039-2
8	906	68.2	296	5	US-09-949-039-75
9	900	67.7	252	1	PCT-US02-11474-73
10	900	67.7	252	6	US-10-120-414-73
11	878.5	66.1	245	6	US-10-039-785-42
12	878.5	66.1	245	6	US-10-139-785-42
13	868.5	65.3	245	6	US-10-039-785-46
14	868.5	65.3	245	6	US-10-139-785-46
15	863.5	65.0	245	6	US-10-039-785-49
16	863.5	65.0	245	6	US-10-139-785-49
17	862	64.9	252	1	PCT-US02-16106-14
18	862	64.9	252	6	US-10-151-882-14
19	859.5	64.7	245	6	US-10-039-785-48
20	859.5	64.7	245	6	US-10-139-785-48
21	858	64.6	224	5	US-09-791-537-128090
22	857	64.5	254	1	PCT-US02-16106-24
23	857	64.5	254	6	US-10-151-882-24
24	856.5	64.4	245	6	US-10-039-785-47
25	856.5	64.4	245	6	US-10-139-785-47
26	855.5	64.4	224	5	US-09-791-537-128088

27	853.5	64.2	245	6	US-10-039-785-43	Sequence 43, Appl
28	853.5	64.2	245	6	US-10-139-785-43	Sequence 43, Appl
29	850.5	64.0	245	6	US-10-039-785-51	Sequence 51, Appl
30	850.5	64.0	245	6	US-10-139-785-51	Sequence 51, Appl
31	849.5	63.9	232	5	US-09-791-537-128053	Sequence 128053,
32	841	63.3	252	1	PCT-US02-16106-13	Sequence 13, Appl
33	841	63.3	252	6	US-10-151-882-13	Sequence 13, Appl
34	839.5	63.2	245	6	US-10-039-785-45	Sequence 45, Appl
35	839.5	63.2	245	6	US-10-139-785-45	Sequence 45, Appl
36	832.5	62.6	245	1	PCT-US02-16106-15	Sequence 15, Appl
37	832.5	62.6	245	6	US-10-151-882-15	Sequence 15, Appl
38	831.5	62.6	227	5	US-09-791-537-128067	Sequence 128067,
39	831.5	62.6	249	5	US-09-959-373A-2	Sequence 2, Appli
40	831	62.5	248	1	PCT-US02-16106-19	Sequence 19, Appl
41	831	62.5	248	6	US-10-151-882-19	Sequence 19, Appl
42	818.5	61.6	245	6	US-10-039-785-52	Sequence 52, Appl
43	818.5	61.6	245	6	US-10-139-785-52	Sequence 52, Appl
44	814.5	61.3	235	1	PCT-US02-11474-82	Sequence 82, Appl
45	814.5	61.3	235	6	US-10-120-414-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1
US-09-791-537-39412
; Sequence 39412, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39412
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-39412

Query Match	82.9%	Score	1101.5;	DB	5;	Length	262;
Best Local Similarity	85.6%	Pred. No.	1.3e-60;				
Matches	214;	Conservative	8;	Mismatches	19;	Indels	9;
Gaps	2;						
QY	1	EVQLVQSGAEVKKPGASVKV	SKCKASGYTFTGYMYWVRQAPQGQGLEWMGWINPNSGGTNY	60			
Db	3	QVQLVQSGAEVKKPGASVKV	SKCKASGYTFTSYAMHWVRQAPQGRLEWMGWINAGNNTKY	62			
QY	61	AQKFGQGRVTMRDTSIGTAYMEL	SRLSSDDTAVVYCAR-DRYYGSSAYHRGSYYMDVWGR	119			
Db	63	SQKFGQGRVTITRDTASTAYMEL	SSLRSEDVAVVYCARLTRNKFKSRGH-----WGQ	114			
QY	120	GTLVTVSSGGGTGGGGGGGGSS	ELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOK	179			
Db	115	GTLVTVSRGGGGGGGGGGGGSS	ELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOK	174			
QY	180	PGQAPVLVIYCKNNRPSGIPDR	FGSSSGNTASLTITGAQAEADYICNSRDSSGNHVV	239			
Db	175	PGQAPVLVIYCKNNRPSGIPDR	FGSSSGNTASLTITGAQAEADYICNSRDSSGNHVV	234			
QY	240	FGGGTKLTVL	249				
Db	235	FGGGTKLTVL	244				

RESULT 2
US-09-791-537-121575
; Sequence 121575, Application US/09791537

; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 121575
; LENGTH: 262
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-121575

Query Match 82.7%; Score 1098.5; DB 5; Length 262;
Best Local Similarity 85.5%; Pred. No. 2e-60;
Matches 213; Conservative 9; Mismatches 20; Indels 7; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYVVRQAPGQGLEWMGWINPNSGGTNY 60
Db 3 QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYVVRQAPGQGLEWMGWINAGNNTKY 62

QY 61 AQKFQGRVTMTDTSIGTAYMELSRLLSSDDTAVYYCARDRIYGGSSAYHRGSIYMDVWGRG 120
Db 63 SQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCA--RLTPNKFKSRGH-----WGQG 115

QY 121 TLVTSSGGGGTGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180
Db 116 TLVTVSRGGGGGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 175

QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 240
Db 176 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 235

QY 241 GGGTKLTVL 249
Db 236 GGGTKLTVL 244

RESULT 3
PCT-US02-16106-20
; Sequence 20, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A030D09 scFv
PCT-US02-16106-20

Query Match 81.0%; Score 1076; DB 1; Length 250;
Best Local Similarity 83.5%; Pred. No. 4.6e-59;
Matches 208; Conservative 11; Mismatches 30; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYVVRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 QVQLQSGAEVKKPGSSVKVCKTSGGAFSHYAIHWVRLAPGQGLEWMGDIIPVYGSTTY 60

QY 61 AQKFQGRVTMTDTSIGTAYMELSRLLSSDDTAVYYCARDRIYGGSSAYHRGSIYMDVWGRG 120
Db 61 AQKFQDRVTISADESTSTAYMELSSLRSEDTAVYYCARSWYYDILTYWYDYYMDVWVGKG 120

QY 121 TLVTSSGGGGTGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180
Db 121 TLVTSSGGGGGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180

QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 240
Db 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 240

QY 241 GGGTKLTVL 249
Db 241 GGGTKLTVL 249

RESULT 4
US-10-151-882-20
; Sequence 20, Application US/10151882
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A030D09 scFv
US-10-151-882-20

Query Match 81.0%; Score 1076; DB 6; Length 250;
Best Local Similarity 83.5%; Pred. No. 4.6e-59;
Matches 208; Conservative 11; Mismatches 30; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYVVRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 QVQLQSGAEVKKPGSSVKVCKTSGGAFSHYAIHWVRLAPGQGLEWMGDIIPVYGSTTY 60

QY 61 AQKFQGRVTMTDTSIGTAYMELSRLLSSDDTAVYYCARDRIYGGSSAYHRGSIYMDVWGRG 120
Db 61 AQKFQDRVTISADESTSTAYMELSSLRSEDTAVYYCARSWYYDILTYWYDYYMDVWVGKG 120

QY 121 TLVTSSGGGGTGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180
Db 121 TLVTSSGGGGGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180

QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 240
Db 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 240

QY 241 GGGTKLTVL 249
Db 241 GGGTKLTVL 249

RESULT 5
US-09-791-537-1444
; Sequence 1444, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1444
LENGTH: 262
TYPE: PRT
ORGANISM: synthetic construct
US-09-791-537-1444

Query Match 72.8%; Score 967.5; DB 5; Length 262;
Best Local Similarity 73.5%; Pred. No. 2.2e-52;
Matches 183; Conservative 26; Mismatches 33; Indels 7; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYVWRQAPGGQGLEWMGWINPNSGGTNY 60
Db 3 EVQLVESGGGLVPGGSLRLSCAASGFTFSYMSWIRQAPGKLEWVSYSISGGSTIYY 62
QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLRLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120
Db 63 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARH---PGRMFRSPY---WGQG 115
QY 121 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 180
Db 116 TLVTVSRGGGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 175
QY 181 GOAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240
Db 176 GOAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 235
QY 241 GGGTKLTIVL 249
Db 236 GGGTKLTIVL 244

RESULT 6
US-09-791-537-118537
Sequence 118537, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 118537
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-118537

Query Match 69.9%; Score 928.5; DB 5; Length 253;
Best Local Similarity 72.3%; Pred. No. 5.3e-50;
Matches 180; Conservative 23; Mismatches 31; Indels 15; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYVWRQAPGGQGLEWMGWINPNSGGTNY 60
Db 2 EVQLVESGGGLIQGGSLRLSCAASGFTVSSNYSWVRQAPGKLEWVSIIY-SGGSTIYY 60
QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLRLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVLLCKRD-----LCDWGQG 106
QY 121 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 180
Db 107 TLVTVSRGGGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 166

QY 181 GOAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240
Db 167 GOAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 226
QY 241 GGGTKLTIVL 249
Db 227 GGGTKLTIVL 235

RESULT 7
US-09-949-039-2
Sequence 2, Application US/09949039
GENERAL INFORMATION:
APPLICANT: HAWLEY, STEPHEN B.
TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
FILE REFERENCE: 057220/1301
CURRENT APPLICATION NUMBER: US/09/949,039
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 290
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pSyn5Af amino
OTHER INFORMATION: acid sequence
US-09-949-039-2

Query Match 68.2%; Score 906; DB 5; Length 290;
Best Local Similarity 68.3%; Pred. No. 1.4e-48;
Matches 170; Conservative 37; Mismatches 32; Indels 10; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYVWRQAPGGQGLEWMGWINPNSGGTNY 60
Db 28 QVQLVQSGGGVYVQPGRLSLRSCAASGFTFSYAMHWVRQAPGKLEWVSATSGSGSTYY 87
QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLRLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120
Db 88 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDT-----RG--YFDLWGRG 137
QY 121 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 180
Db 138 TLVTVSSGGGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQRP 197
QY 181 GOAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240
Db 198 RQAPRLVVIYGNKRRPSGIPERFSGTSGDTASLTISGLQAEDEADYYCHSRDSNADLVVF 257
QY 241 GGGTKLTIVL 249
Db 258 GGGTKVTIVL 266

RESULT 8
US-09-949-039-75
Sequence 75, Application US/09949039
GENERAL INFORMATION:
APPLICANT: HAWLEY, STEPHEN B.
TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
FILE REFERENCE: 057220/1301
CURRENT APPLICATION NUMBER: US/09/949,039
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 75
LENGTH: 296
TYPE: PRT
ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sFv5AF-Cys amino
; OTHER INFORMATION: acid sequence
US-09-949-039-75

Query Match      68.2%; Score 906; DB 5; Length 296;
Best Local Similarity 68.3%; Pred. No. 1.4e-48;
Matches 170; Conservative 37; Mismatches 32; Indels 10; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   :|||||  | :|| |::|| ||||::| |::| |||||::| ||| : | | |
Db 28 QVQLVQSGGVVQPGRLSLRSCAASGFTFSSYAMHWVRQAPGKGLEWVSAISGSGSTYY 87
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAYHRGSYYMDVWGR 120
   | :|| | | | | : : |::: | : ||||| | | | | | | | | | | | |
Db 88 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDT-----RG--YFDLWGRG 137
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TLVTVSSGGGGTGGGGGGGSSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQOKP 180
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 138 TLVTVSSGGGGGGGGGGGSSSELTQDPAMSVLALGQTVRITCQGDSLRSYHASNWYQOKP 197
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 GQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSNGHHVF 240
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 198 RQAPRLVYVYGNKNNRPSGIPDRFSGTSGDTASLTISGLQAEADYYCHSRDSNADLVVF 257
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 GGGTKLTVL 249
   ||||| | | |
Db 258 GGGTKVTVL 266

RESULT 9
PCT-US02-11474-73
; Sequence 73, Application PC/Tus0211474
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF1129PCT
; CURRENT APPLICATION NUMBER: PCT/US02/11474
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,385
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/350,366
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-11474-73

Query Match      67.7%; Score 900; DB 1; Length 252;
Best Local Similarity 70.4%; Pred. No. 2.9e-48;
Matches 178; Conservative 25; Mismatches 44; Indels 6; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   ::||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 QMQLVQSGAEVKKPGSSVKVSCKASGGIFSSYAISWVRQAPGQGLEWMGGIIPRFGTANY 60
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAY-HRGSYYMDVWGR 119
   ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 61 AQKFEGRVTITADESTAYMELSSLRSEDVAVYYCARDQVRASGSYPYYYYYMDVWQG 120
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 120 GTLVTVSSGGGGTGGGGGGGSS--ELTQDPAVSVALGQTVRITCQGDSLRSYYASWY 176
   ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 121 GTLVTVSSGGGGGGGGGGSALSIVLTQPPSMVSVPQTARITCSGDKLGDKYASWY 180
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 QOKPQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSNG 236
   ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 181 QOKPQSPVLVIYQDSERPSPGIPERFSGSNSGNTATLTIRGTQPLDEADYYCQTWDTSTG 240
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 237 HVVFGGGTKLTVL 249
   ||||| | | |
Db 241 --VFGGTQLTVL 251

RESULT 11
US-10-039-785-42
; Sequence 42, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
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QY 237 HVVFGGGTKLTVL 249
   ||||| | | |
Db 241 --VFGGTQLTVL 251

RESULT 10
US-10-120-414-73
; Sequence 73, Application US/10120414
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P9
; CURRENT APPLICATION NUMBER: US/10/120,414
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,385
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/350,366
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-414-73

Query Match      67.7%; Score 900; DB 6; Length 252;
Best Local Similarity 70.4%; Pred. No. 2.9e-48;
Matches 178; Conservative 25; Mismatches 44; Indels 6; Gaps 3;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   ::||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 QMQLVQSGAEVKKPGSSVKVSCKASGGIFSSYAISWVRQAPGQGLEWMGGIIPRFGTANY 60
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLSSDDTAVYYCARDRIYGYSSAY-HRGSYYMDVWGR 119
   ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 61 AQKFEGRVTITADESTAYMELSSLRSEDVAVYYCARDQVRASGSYPYYYYYMDVWQG 120
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 120 GTLVTVSSGGGGTGGGGGGGSS--ELTQDPAVSVALGQTVRITCQGDSLRSYYASWY 176
   ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 121 GTLVTVSSGGGGGGGGSALSIVLTQPPSMVSVPQTARITCSGDKLGDKYASWY 180
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 QOKPQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSNG 236
   ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db 181 QOKPQSPVLVIYQDSERPSPGIPERFSGSNSGNTATLTIRGTQPLDEADYYCQTWDTSTG 240
   :||| | | | | | | | | | | | | | | | | | | | | | | | |
QY 237 HVVFGGGTKLTVL 249
   ||||| | | |
Db 241 --VFGGTQLTVL 251

RESULT 11
US-10-039-785-42
; Sequence 42, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
```

```
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A04 scFv
US-10-039-785-42

Query Match          66.1%; Score 878.5; DB 6; Length 245;
Best Local Similarity 68.1%; Pred. No. 6e-47;
Matches 173; Conservative 28; Mismatches 38; Indels 15; Gaps 6;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   |||||:|||||:|||||: ||: ||: |||||: |||||: |||||: |||||: |||||:
Db 1 EVQLVQSGADVKKRPASVKVSKISGDSFNAYFIHWVRQAPGQGLEWMGFNPDSTADS 60

QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLRLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120
   |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 61 AQKFGHGRVTMTSDTSSTAFLELSRLSRDSDTAVYYCVRQ-----HRGNTFAP-WGRG 111

QY 121 TLVTVSSGGGTGGGGGGSSSE--LTQDPAVSVALGQTVRITCQG--DSLRSY-YASW 175
   |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 121 TMVTVSSGGGTGGGGGGSSAQSVLTQPPSASGSPGQSVTISCTGTTSDVGGYNYVSW 171

QY 176 YQQKPGQAPVLIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG 235
   |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 176 YQQHPGKAPKLMYGVNQRPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYYCSSYAGS- 230

QY 236 NHVVFSGGTGKLTVL 249
   |: |||||: |||||
Db 231 NNWVFSGGTGKLTVL 244

RESULT 12
US-10-139-785-42
; Sequence 42, Application US/10139785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014B01 scFv
US-10-039-785-46
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; SEQ ID NO 42
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A04 scFv
US-10-139-785-42

Query Match          66.1%; Score 878.5; DB 6; Length 245;
Best Local Similarity 68.1%; Pred. No. 6e-47;
Matches 173; Conservative 28; Mismatches 38; Indels 15; Gaps 6;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
   |||||:|||||:|||||: ||: ||: |||||: |||||: |||||: |||||: |||||:
Db 1 EVQLVQSGADVKKRPASVKVSKISGDSFNAYFIHWVRQAPGQGLEWMGFNPDSTADS 60

QY 61 AQKFGQGRVTMTSDTSIGTAYMELSLRLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120
   |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 61 AQKFGHGRVTMTSDTSSTAFLELSRLSRDSDTAVYYCVRQ-----HRGNTFAP-WGRG 111

QY 121 TLVTVSSGGGTGGGGGGSSSE--LTQDPAVSVALGQTVRITCQG--DSLRSY-YASW 175
   |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 121 TMVTVSSGGGTGGGGGGSSAQSVLTQPPSASGSPGQSVTISCTGTTSDVGGYNYVSW 171

QY 176 YQQKPGQAPVLIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG 235
   |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 176 YQQHPGKAPKLMYGVNQRPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYYCSSYAGS- 230

QY 236 NHVVFSGGTGKLTVL 249
   |: |||||: |||||
Db 231 NNWVFSGGTGKLTVL 244

RESULT 13
US-10-039-785-46
; Sequence 46, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014B01 scFv
US-10-039-785-46
```



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Query Match          65.3%; Score 868.5; DB 6; Length 245;
Best Local Similarity 68.1%; Pred. NO. 2.5e-46;
Matches 173; Conservative 28; Mismatches 38; Indels 15; Gaps 6;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFGTGYMYVVRQAPGGQGLEWMGWINPNSGGTNY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKPGASVKVCKISGDTFAAYFIHWVRQAPGQGLEWMGFNPGTADS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFQGRVTMTSDTSGTAYMELSLRLSSDDTAVYYCARDRIYGSAYHRCGYMDVWGRG 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SQKFHGRVTMTSDTSGTAYMELSLRLSDDTAVYYCARQ-----HRSNTFF-DPWGQG 111

QY 121 TLVTVSSGGGTGGGGSSSE--LTQDPAVSVALGQTVRITCQGDS--LRSY-YASW 175
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TMVTVSSGGGTGGGGSSAQSVVTPPPSVSGSPGQSVTISCTGTSSDIGAYNYVSW 171

QY 176 YQOKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG 235
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FQOHGPKAPKLIIEVSKRPSGVPDRLSGSKSGNTASLTVSGLQAEDEADYYCGSYAGS- 230

QY 236 NHVFGGGTKLTVL 249
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 NIWVFGGTKVTVL 244

RESULT 14
US-10-139-785-46
; Sequence 46, Application US/10139785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 46
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014B01 scfv
US-10-139-785-46

Query Match          65.3%; Score 868.5; DB 6; Length 245;
Best Local Similarity 68.1%; Pred. NO. 2.5e-46;
Matches 173; Conservative 28; Mismatches 38; Indels 15; Gaps 6;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFGTGYMYVVRQAPGGQGLEWMGWINPNSGGTNY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKPGASVKVCKISGDTFAAYFIHWVRQAPGQGLEWMGFNPGTADS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFQGRVTMTSDTSGTAYMELSLRLSSDDTAVYYCARDRIYGSAYHRCGYMDVWGRG 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SQKFHGRVTMTSDTSGTAYMELSLRLSDDTAVYYCARQ-----HRSNTFF-DPWGQG 111

QY 121 TLVTVSSGGGTGGGGSSSE--LTQDPAVSVALGQTVRITCQGDS--LRSY-YASW 175
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TMVTVSSGGGTGGGGSSAQSVVTPPPSVSGSPGQSVTISCTGTSSDIGAYNYVSW 171

QY 176 YQOKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG 235
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FQOHGPKAPKLIIEVSKRPSGVPDRLSGSKSGNTASLTVSGLQAEDEADYYCGSYAGS- 230

QY 236 NHVFGGGTKLTVL 249
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 NIWVFGGTKVTVL 244
```

```
Db 61 SQKFHGRVTMTSDTSGTAYMELSLRLSDDTAVYYCARQ-----HRSNTFF-DPWGQG 111
QY 121 TLVTVSSGGGTGGGGSSSE--LTQDPAVSVALGQTVRITCQGDS--LRSY-YASW 175
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 TMVTVSSGGGTGGGGSSAQSVVTPPPSVSGSPGQSVTISCTGTSSDIGAYNYVSW 171
QY 176 YQOKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG 235
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FQOHGPKAPKLIIEVSKRPSGVPDRLSGSKSGNTASLTVSGLQAEDEADYYCGSYAGS- 230
QY 236 NHVFGGGTKLTVL 249
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 NIWVFGGTKVTVL 244

RESULT 15
US-10-039-785-49
; Sequence 49, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 49
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014G04 scfv
US-10-039-785-49

Query Match          65.0%; Score 863.5; DB 6; Length 245;
Best Local Similarity 67.7%; Pred. NO. 5e-46;
Matches 172; Conservative 30; Mismatches 37; Indels 15; Gaps 6;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYTFGTGYMYVVRQAPGGQGLEWMGWINPNSGGTNY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVQSGADVKKRPGASVKVCKISGDSFTAYFIHWVRQAPGQGLEWMGFNPGTADS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFQGRVTMTSDTSGTAYMELSLRLSSDDTAVYYCARDRIYGSAYHRCGYMDVWGRG 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFHGRVTMTSDTSSSTAFLSLRLSDDTAVYYCVRQ-----HRCNTFAP-WGRG 111

QY 121 TLVTVSSGGGTGGGGSSSE--LTQDPAVSVALGQTVRITCQGDS--LRSY-YASW 175
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 TLVTVSSGGGTGGGGSSAQSVVLTQPPSASGSPGQSVTISCTGTSSDVGSYEYVSW 171
QY 176 YQOKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG 235
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 172 YQHPGKAPRLMISEVNKRPSGVPNRFSGSKSGNTASLTVSGLQADDEADYYCSSYAGS - 230

Qy 236 NHVVFSGGKLTJVL 249

I: |||||: ||

Db 231 NNWVFSGGKVTJVL 244

Search completed: August 15, 2002, 16:27:06
Job time: 371 sec

Db 233 GGGTKLTVL 241

RESULT 15

US-09-880-748-2021
; Sequence 2021, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2021
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2021

Query Match		88.6%	Score 1177;	DB 22;	Length 242;
Best Local Similarity		89.6%	Pred. No. 8.8e-98;		
Matches	223;	Conservative	8;	Mismatches	10;
				Indels	8;
				Gaps	1;
QY	1	EVQLVQSGAEVKKPGASVKVSCKASGYTF	GYMYWVRQAPGGGLEWMGWINPNSGGTNY	60	
Db	1	QVNLRESGAEVKKPGASVKVSCKASGYTF	GYMYWVRQAPGGGLEWMGWINPNSGGTNY	60	
QY	61	AQKFOGRVTMTTRDTSIGTAYMELSR	LSSDDTAVYYCARDYYGSSAYHRGSYYMDVWGRG	120	
Db	61	AQKFOGRVTMTTRDTSIS	TAYMELSR	LSSDDTAVYYCAREDLTGDA-----FDIWGRS	112
QY	121	TLVTYSSGGGGTGGGGGGSSSELTQDP	AVSVALGQTVRITCGDSLRSYYASWYQQKP	180	
Db	113	TLVTYSSGGGGGGGGSSSELTQNP	AVSVALGQTVRITCGDSLRSYYASWYQQKP	172	
QY	181	GQAPVLVIYGNRRPSGIPDRFSSSSSGNT	ASLTITGAQAEDEADYYCNSRDS	SGNHVVF 240	
Db	173	GQAPVLVIYGNRRPSGIPDRFSSSSSGNT	ASLTITGAQAEDEADYYCNSRDS	SGNHVVF 232	
QY	241	GGGTKLTVL	249		
Db	233	GGGTKLTVL	241		

Search completed: August 15, 2002, 16:34:04
Job time: 764 sec

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; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2014
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2014

Query Match      88.9%; Score 1181.5; DB 1; Length 243;
Best Local Similarity 90.0%; Pred. No. 3.5e-98;
Matches 224; Conservative 8; Mismatches 10; Indels 7; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGGQGLEWMGWINPNSGGTNY 60
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1 QVNLRESGAEVKKPGASVKVSCKASGYTFGTGYMHVVRQAPGGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQGRVTMTTRDTSIGTAYMELSLRSSDDTAVYYCARDRIYGYSSAYHRGSYMDVWGRG 120
||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 61 AQKFGQGRVTMTTRDTSISITAYMELSLRLSDDTAVYYCARELTGANDAF-----DIWGRS 113

QY 121 TLVTVSSGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 114 TLVTVSSGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 173

QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240
||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 174 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 233

QY 241 GGGTKLTVL 249
|||||
Db 234 GGGTKLTVL 242

RESULT 13
US-09-880-748-2014
; Sequence 2014, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2014
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2014

Query Match      88.9%; Score 1181.5; DB 22; Length 243;
Best Local Similarity 90.0%; Pred. No. 3.5e-98;
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```

Matches 224; Conservative 8; Mismatches 10; Indels 7; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGGQGLEWMGWINPNSGGTNY 60
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1 QVNLRESGAEVKKPGASVKVSCKASGYTFGTGYMHVVRQAPGGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQGRVTMTTRDTSIGTAYMELSLRSSDDTAVYYCARDRIYGYSSAYHRGSYMDVWGRG 120
||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 61 AQKFGQGRVTMTTRDTSISITAYMELSLRLSDDTAVYYCARELTGANDAF-----DIWGRS 113

QY 121 TLVTVSSGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 114 TLVTVSSGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 173

QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240
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Db 174 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 233

QY 241 GGGTKLTVL 249
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Db 234 GGGTKLTVL 242

RESULT 14
PCT-US01-19110-2021
; Sequence 2021, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2021
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2021

Query Match      88.6%; Score 1177; DB 1; Length 242;
Best Local Similarity 89.6%; Pred. No. 8.8e-98;
Matches 223; Conservative 8; Mismatches 10; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGGQGLEWMGWINPNSGGTNY 60
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Db 1 QVNLRESGAEVKKPGASVKVSCKASGYTFGTGYMHVVRQAPGGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQGRVTMTTRDTSIGTAYMELSLRSSDDTAVYYCARDRIYGYSSAYHRGSYMDVWGRG 120
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Db 61 AQKFGQGRVTMTTRDTSISITAYMELSLRLSDDTAVYYCARELTGDA-----FDIWGRS 112

QY 121 TLVTVSSGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
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Db 113 TLVTVSSGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 172

QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240
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Db 173 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 232

QY 241 GGGTKLTVL 249
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1722

Query Match      89.3%; Score 1187; DB 22; Length 250;
Best Local Similarity 90.8%; Pred. No. 1.1e-98;
Matches 228; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
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Db 1 QVQLQESGAEVKKPGASVKVSCKASGYTFGTGYMHVVRQAPGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSLSSDDTAVYYCAR--DRYYGSSAYHRGSYYMDVWG 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFQGRVTMTTRDTSISITAYMELSLRSSDDTAVYYCARVLPHYDILTGYSON--WFDPWG 118

QY 119 RGTLVTVSSGGGGTGGGGGGSSSELTDQPAVSVALGQTVRITCQGDSLSRYYASWYQQ 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 119 RGTLVTVSSGGGGGGGGSSSELTDQPAVSVALGQTVRITCQGDSLSRYYASWYQQ 178

QY 179 KPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGHNH 238
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Db 179 KPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGHNH 238

QY 239 VFGGSKLTIVL 249
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Db 239 VFGGSKLTIVL 249

RESULT 10
PCT-US01-19110-2008
; Sequence 2008, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2008
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2008

Query Match      89.0%; Score 1182.5; DB 22; Length 241;
Best Local Similarity 90.0%; Pred. No. 2.8e-98;
Matches 224; Conservative 8; Mismatches 8; Indels 9; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
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Db 1 QVQLQESGAEVKKPGASVKVSCKASGYTFGTGYMHVVRQAPGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFQGRVTMTTRDTSIGTAYMELSLSSDDTAVYYCARDRYGSSAYHRGSYYMDVWGRG 120
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Db 61 AQKFQGRVTMTTRDTSISITAYMELSLRSSDDTAVYYCARG-----AGSRYFDLWGQS 111

QY 121 TLVTVSSGGGGTGGGGGGSSSELTDQPAVSVALGQTVRITCQGDSLSRYYASWYQQKP 180
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Db 112 TLVTVSSGGGGGGGGSSSELTDQPAVSVALGQTVRITCQGDSLSRYYASWYQQKP 171

QY 181 GOAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGHNHVF 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 172 GOAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCHSRDSSGHNHVL 231

QY 241 GGGTKLTIVL 249
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Db 232 GGGTKLTIVL 240

RESULT 12
PCT-US01-19110-2014
; Sequence 2014, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
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Db 234 GGGTKLTVL 242

RESULT 4

PCT-US01-19110-2106

; Sequence 2106, Application PC/TUS0119110

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523PCT

; CURRENT APPLICATION NUMBER: PCT/US01/19110

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2106

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US01-19110-2106

Query Match 89.5%; Score 1189; DB 1; Length 242;

Best Local Similarity 90.4%; Pred. No. 7.3e-99;

Matches 225; Conservative 7; Mismatches 9; Indels 8; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYFTFTGYMYWVRQAPGGQGLEWMGWINPNSGGTNY 60

Db 1 QVQLQESGAEVKKPGASVKVCKASGYFTFTGYMHVVRQAPGGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120

Db 61 AQKFGQGRVTMTDTSISTAYMELSLRLSDDTAVYYCARESLTGDA-----FDIWGRS 112

QY 121 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 180

Db 113 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 172

QY 181 GQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240

Db 173 GQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 232

QY 241 GGGTKLTVL 249

Db 233 GGGTKLTVL 241

RESULT 5

US-09-880-748-2106

; Sequence 2106, Application US/09880748

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523

; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2106

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-748-2106

Query Match 89.5%; Score 1189; DB 22; Length 242;

Best Local Similarity 90.4%; Pred. No. 7.3e-99;

Matches 225; Conservative 7; Mismatches 9; Indels 8; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKVCKASGYFTFTGYMYWVRQAPGGQGLEWMGWINPNSGGTNY 60

Db 1 QVQLQESGAEVKKPGASVKVCKASGYFTFTGYMHVVRQAPGGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQGRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRIYGGSSAYHRGSYYMDVWGRG 120

Db 61 AQKFGQGRVTMTDTSISTAYMELSLRLSDDTAVYYCARESLTGDA-----FDIWGRS 112

QY 121 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 180

Db 113 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYYASWYQQKP 172

QY 181 GQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 240

Db 173 GQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF 232

QY 241 GGGTKLTVL 249

Db 233 GGGTKLTVL 241

RESULT 6

PCT-US01-19110-2046

; Sequence 2046, Application PC/TUS0119110

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523PCT

; CURRENT APPLICATION NUMBER: PCT/US01/19110

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2046

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US01-19110-2046

Query Match 89.3%; Score 1187; DB 1; Length 242;

Best Local Similarity 90.3%; Pred. No. 1.1e-98;

Matches 224; Conservative 7; Mismatches 9; Indels 8; Gaps 1;

QY 2 VQLVQSGAEVKKPGASVKVCKASGYFTFTGYMYWVRQAPGGQGLEWMGWINPNSGGTNYA 61

Db 2 VQLVESGAEVKRPGASVKVCKASGYFTFTGYMHVVRQVPGQGLEWMGWINPNSGGTNYA 61

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 16:34:03 ; Search time 410.32 Seconds
(without alignments)
213.597 Million cell updates/sec

Title: US-08-779-457-48
Perfect score: 1329
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1329	100.0	249	11 US-08-779-457-48	Sequence 48, Appl
2	1191.5	89.7	243	1 PCT-US01-19110-2107	Sequence 2107, Ap
3	1191.5	89.7	243	22 US-09-880-748-2107	Sequence 2107, Ap
4	1189	89.5	242	1 PCT-US01-19110-2106	Sequence 2106, Ap
5	1189	89.5	242	22 US-09-880-748-2106	Sequence 2106, Ap
6	1187	89.3	242	1 PCT-US01-19110-2046	Sequence 2046, Ap
7	1187	89.3	242	22 US-09-880-748-2046	Sequence 2046, Ap

8	1187	89.3	250	1 PCT-US01-19110-1722	Sequence 1722, Ap
9	1187	89.3	250	22 US-09-880-748-1722	Sequence 1722, Ap
10	1182.5	89.0	241	1 PCT-US01-19110-2008	Sequence 2008, Ap
11	1182.5	89.0	241	22 US-09-880-748-2008	Sequence 2008, Ap
12	1181.5	88.9	243	1 PCT-US01-19110-2014	Sequence 2014, Ap
13	1181.5	88.9	243	22 US-09-880-748-2014	Sequence 2014, Ap
14	1177	88.6	242	1 PCT-US01-19110-2021	Sequence 2021, Ap
15	1177	88.6	242	22 US-09-880-748-2021	Sequence 2021, Ap
16	1173	88.3	250	1 PCT-US01-19110-1723	Sequence 1723, Ap
17	1173	88.3	250	22 US-09-880-748-1723	Sequence 1723, Ap
18	1170.5	88.1	241	1 PCT-US01-19110-2032	Sequence 2032, Ap
19	1170.5	88.1	241	22 US-09-880-748-2032	Sequence 2032, Ap
20	1169.5	88.0	241	1 PCT-US01-19110-2031	Sequence 2031, Ap
21	1169.5	88.0	241	22 US-09-880-748-2031	Sequence 2031, Ap
22	1167	87.8	248	1 PCT-US01-19110-1721	Sequence 1721, Ap
23	1167	87.8	248	22 US-09-880-748-1721	Sequence 1721, Ap
24	1162.5	87.5	238	1 PCT-US01-19110-1907	Sequence 1907, Ap
25	1162.5	87.5	238	22 US-09-880-748-1907	Sequence 1907, Ap
26	1158.5	87.2	247	1 PCT-US01-19110-1729	Sequence 1729, Ap
27	1158.5	87.2	247	22 US-09-880-748-1729	Sequence 1729, Ap
28	1150.5	86.6	245	1 PCT-US01-19110-1919	Sequence 1919, Ap
29	1150.5	86.6	245	22 US-09-880-748-1919	Sequence 1919, Ap
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31	1145.5	86.2	249	22 US-09-880-748-2033	Sequence 2033, Ap
32	1145	86.2	250	1 PCT-US01-19110-1647	Sequence 1647, Ap
33	1145	86.2	250	22 US-09-880-748-1647	Sequence 1647, Ap
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35	1143.5	86.0	247	22 US-09-880-748-927	Sequence 927, App
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37	1142.5	86.0	247	22 US-09-880-748-948	Sequence 948, App
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39	1138	85.6	248	22 US-09-880-748-967	Sequence 967, App
40	1137.5	85.6	243	1 PCT-US01-19110-1947	Sequence 1947, Ap
41	1137.5	85.6	243	22 US-09-880-748-1947	Sequence 1947, Ap
42	1136	85.5	246	1 PCT-US01-19110-1638	Sequence 1638, Ap
43	1136	85.5	246	22 US-09-880-748-1638	Sequence 1638, Ap
44	1135.5	85.4	249	1 PCT-US01-19110-1730	Sequence 1730, Ap
45	1135.5	85.4	249	22 US-09-880-748-1730	Sequence 1730, Ap

ALIGNMENTS

RESULT 1
US-08-779-457-48
; Sequence 48, Application US/08779457
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96

Best Local Similarity 46.9%; Pred. NO. 1.3e-21;
Matches 83; Conservative 25; Mismatches 38; Indels 31; Gaps 4;

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Job time: 797 sec

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RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yanashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT *NEDO human cDNA sequencing project.*;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058027; BAB71633.1; -.
SQ SEQUENCE 496 AA; 53532 MW; C72BE1E247C86FED CRC64;

Query Match 30.5%; Score 396.5; DB 4; Length 496;
Best Local Similarity 40.8%; Pred. No. 2e-22;
Matches 102; Conservative 27; Mismatches 82; Indels 39; Gaps 8;

QY 1 EVQLVQSGAEVKKPGESLKISQCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVHLVQSGAELKNGSSVKVSCKASANMFRSYAFTWVRQAPGQGLQWNGGIIPFGAPNY 79

QY 61 AQKFQGRVTTTADSTSTAYMELSSLRSEDTAVVYCARDRVVVPATSLRGMDVWGQGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 AONFQDRVTTISADSTTTVMELTSLTFEDFAFYCGRGLTYYGSGSY-YLQHWGQGT 138

QY 121 VTVSSGGGGGGGGGGSGSVLTQPAV-SGSPGQSITISCTGTSDDYGGYVSWYQ 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 139 VTVSS-----ASPTSPKVFLSLCSTQPDGNVVIACL-----VQGF----FP 176

QY 180 QHPGKAPKLMYEGSKRPSGVSNR-----FSGSKSGSTASLTISGLQ--AEDEADYYC 230
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 177 QEP-----LSVTWSESGQGVTAARNFPPSQDASGDLTYTSSQLTLPATQCLAGKSVTCHV 230

QY 231 SSYTTRSTRV 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 231 KHYTNPSQDV 240

RESULT 14
QY9298 ID QY9298 PRELIMINARY; PRT; 150 AA.
AC QY9298;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAAL1829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;
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Query Match 29.8%; Score 388; DB 4; Length 150;
Best Local Similarity 62.4%; Pred. No. 2.2e-22;
Matches 78; Conservative 15; Mismatches 24; Indels 8; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISQCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLVQSGAEVKKPGASVKVSGYTLTELPVHWVGOAPGKGLEWVGSFDPESGESIY 79

QY 61 AQKFQGRVTTTADSTSTAYMELSSLRSEDTAVVYCARDRVVVPATSLRGMDVWGQGT 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYCA-----VPDPD---AFDIWGQGT 131

QY 121 VTVSS 125
   |||||
Db 132 VTVSS 136

RESULT 15
QY9D8L4 ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 181006009RIK PROTEIN.
GN IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cdna collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 29.7%; Score 385.5; DB 11; Length 473;
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Db 80 AQKQDRVTITRDRSMNTAYMELSSLRSEDYAMYYCARG-----SSSWDDAFDIWGQGT 135

QY 121 VTVSSGGGGGGGGGSGGGSQSVLTQPASVSGSPG--QSITISCTG----- 164

Db 136 VTVSS-----GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKY 184

QY 165 -TSSDVG-----GYNVSWYQ-----QHPG----- 183

Db 185 KNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMOGTDEHVYCKVQHPNGNKEKNVPLP 244

QY 184 -----KAPKLMY-----EGSKRPSGVSN--- 202

Db 245 VIAELPPKVSFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVSGVYTTDQV 304

QY 203 RFGSKSGS-----TASLTIS-----GLQAEADYYCSSYTTTRSTRV 240

Db 305 QAEAKESGPTTYKVITSTLTIKESDWLSQSMFTCRVDHRGLTFQONASSMCPDQDTAIRV 364

QY 241 FG-----GGTKLTVL 250

Db 365 FAIPPSFASIFLTKSTKLJCL 385

RESULT 11

Q9GYZ2

ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.

AC Q9GYZ2;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;

OC Schistosomatoidea; Schistosomatidae; Schistosoma.

OX NCBI_TaxID=6182;

RN [1]

RP SEQUENCE FROM N.A.

RA Song X.T., Feng Z.Q., Guan X.H.;

RT "Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF282622; AAG01452.1; -.

DR HSSP; P01772; 2FB4.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003600; Ig_like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG_like; 1.

FT NON_TER 1

FT NON_TER 119 119

SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 30.7%; Score 399; DB 5; Length 119;

Best Local Similarity 61.7%; Pred. No. 2.4e-23;

Matches 79; Conservative 16; Mismatches 21; Indels 12; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60

Db 1 QVQLVSGAEVKKPGASVRSCKASGYTFTGYIMNWRQAPGHGLEWIGYINPSRGYTN 60

QY 61 AQKFGQGRVTITADESTSTAYMELSSLRSEDYAVYYCAR--DRVVVPATSLRGGMDVWGQ 117

Db 61 NQKFKDRVTMTDKSFSTAYMDLRLSLRADSASVYICARYDDHYC-----LDYWGQ 111

QY 118 GTTVTVSS 125

Db 112 GTTVTVSS 119

RESULT 12

Q9BRV0

ID Q9BRV0 PRELIMINARY; PRT; 500 AA.

AC Q9BRV0;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE HYPOTHETICAL 54.2 KDA PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PROSTATE;

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC005951; AAH05951.1; -.

DR HSSP; P01789; IMCP.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003600; Ig_like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 4.

DR SMART; SM00409; IG; 4.

DR SMART; SM00407; IGcl; 2.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG_like; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 30.6%; Score 397.5; DB 4; Length 500;

Best Local Similarity 40.4%; Pred. No. 1.7e-22;

Matches 103; Conservative 30; Mismatches 77; Indels 45; Gaps 9;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPGKGLEWMGGIPIFGTANY 60

Db 20 QVHLVQSGAEVMSPGASVRSCKTSGYAFHTYSIIWVRQAPGGGLEWMGWISPSDNTRF 79

QY 61 AQKFGQGRVTITADESTSTAYMELSSLRSEDYAVYYCARDRVVVPATSLRGG-----MDVW 115

Db 80 AKKFGQGRVLTDTSTSTVYMELESLRSDDTAVYYCARR--YCSYSSCQNDYYYVMDVW 137

QY 116 GQGTTVTVSSGGGGGGGGGSGGGSQSVLTQPASV-SGSPGQSITISCTGTSSDVGGYNY 174

Db 138 GKGTTVTVSS-----ASPTSPKVFPPLSLCSTQPDGNVVIACL-----VQGF-- 178

QY 175 VSWYQQHPGKAPKLMYEGSKRPSGVSNR-----FSGSKSGSPASLTISGLQ--AEDE 225

Db 179 ---FPQEP-----LSVTWSESGQGVARNFPPPSQDASGDLYTTSSQLTLPATQCLAGKS 229

QY 226 ADYVCSSYTTTRSTRV 240

Db 230 VTCHVKHYTNPSQDV 244

RESULT 13

Q96DK0

ID Q96DK0 PRELIMINARY; PRT; 496 AA.

AC Q96DK0;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE CDNA FLJ25298 FIS, CLONE STM07683, HIGHLY SIMILAR TO PROTEIN TRO ALPHAI H, MYELOMA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.